

GenCore version 5.1.6  
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4 nucleic - nucleic search, using sw model

in on: April 19, 2004, 15:54:48 ; Search time 0.001 Seconds  
(without alignments)  
1.176 Million cell updates/sec

File: US-10-024-396-3-COPY  
Perfect score: 28  
Sequence: 1 cgggcctacgtacagggagtcagg 28

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Aligned: 2 seqs, 21 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 2000 summaries

Database: esdb:\*

EST

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7.4	26.4	11	1	BM395068
2	7	25.0	10	1	BM393918
3	7	25.0	11	1	BM395068
4	6.4	22.9	10	1	BM393918

#### ALIGNMENTS

Result 1  
BM395068/c

LOCUS 50072-2-7-D04.r.1 Chilcoat/Turkewitz cDNA (large fraction) EST 17-JAN-2002

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM395068

VERSION 1

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.

AUTHORS Frankel, J., and Klobutcher, L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu

Seq primer: T3.  
Location/Qualifiers  
1. .11  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 26.4%; Score 7.4; DB 1; Length 11;  
Best Local Similarity 88.9%; Pred. No. 0;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGGCCCTAC 10  
Db 11 CGGCCCGAC 3

#### RESULT 2

BM393918 10 bp mRNA linear EST 17-JAN-2002  
LOCUS 50072-2-11-H06.r.1 Chilcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM393918

VERSION BM393918.1 GI:18193971

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 10)

AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,

Frankel, J., and Klobutcher, L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu

Seq primer: T3.  
Location/Qualifiers  
1. .10  
/organism="Tetrahymena thermophila"  
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/strain="CU428.1"  
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/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 25.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCCCC 7  
Db 2 CGGCCCC 8

#### RESULT 3

BM395068 11 bp mRNA linear EST 17-JAN-2002  
LOCUS 50072-2-7-D04.r.1 Chilcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM395068

VERSION BM395068.1 GI:18195121

## WORDS

Tetrahymena thermophila  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
1 (bases 1 to 11)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,  
Frankel, J., and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)

## AUTHORS

Contact: Turkewitz AP  
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University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

## FEATURES

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/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## Query Match

Best Local Similarity 25.0%; Score 7; DB 1; Length 11;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGGGCCCC 7

|||||||

5 CGGGCCCC 11

## MULT 4

193918/c  
TUS  
INITIATION  
50072-2-11-H06.r.1 Chilcoat/Turkewitz cDNA (large fraction) linear EST 17-JAN-2002  
Tetrahymena thermophila cDNA, mRNA sequence.

## SESSION

BM393918  
BM393918  
BM393918.1 GI:18193971

## WORDS

Tetrahymena thermophila  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
1 (bases 1 to 10)

## AUTHORS

Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,  
Frankel, J., and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)

## JOURNAL

MENT  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

## FEATURES

1..10 Location/Qualifiers  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 22.9%; Score 6.4; DB 1; Length 10;  
Best Local Similarity 87.5%; Pred. No. 0;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGCCCCA 9

|||||||

Db 8 GGGCCCCA 1

Search completed: April 19, 2004, 15:54:48  
Job time : 0.001 secs

GenCore version 5.1.6  
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4 nucleic - nucleic search, using sw model

in on: April 19, 2004, 14:25:24 ; Search time 0.001 Seconds  
(without alignments)

208.040 Million cell updates/sec

File: US-10-024-396-3-COPY

Effect score: 28

Sequence: 1 cgggcccctacgtgtacagggagtcagg 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Matched: 288 seqs, 3715 residues

Total number of hits satisfying chosen parameters: 576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 301 summaries

Database: rgedb.\* GenEmbl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
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3	18.2	65.0	25	1	AX690107	ACCESSION:AX690107
4	18.2	65.0	25	1	AX690108	ACCESSION:AX690108
5	17.8	63.6	25	1	AX690105	ACCESSION:AX690105
6	17.8	63.6	25	1	AX690106	ACCESSION:AX690106
7	17.6	62.9	25	1	AX690111	ACCESSION:AX690111
8	16.8	60.0	25	1	AX690104	ACCESSION:AX690104
9	16.6	59.3	25	1	AX690112	ACCESSION:AX690112
10	14.4	51.4	17	1	AX688603	ACCESSION:AX688603
11	14.4	51.4	17	1	AX688604	ACCESSION:AX688604
12	14.2	50.7	21	1	AX165205	ACCESSION:AX165205
13	13.8	49.3	17	1	AX688605	ACCESSION:AX688605
14	13.8	49.3	17	1	AX688606	ACCESSION:AX688606
15	13.8	49.3	17	1	AX688607	ACCESSION:AX688607
16	13.8	49.3	17	1	AX688608	ACCESSION:AX688608
17	13.4	47.9	17	1	AX688602	ACCESSION:AX688602
18	13.4	47.9	18	1	AX058208	ACCESSION:AX058208
19	13.4	47.9	18	1	AX143361	ACCESSION:AX143361
20	13.4	47.9	20	1	AX449606	ACCESSION:AX449606
21	13.2	47.1	19	1	ED088466	ACCESSION:ED088466
22	13.2	47.1	19	1	AB065243	ACCESSION:AB065243
23	13.2	47.1	20	1	AX297476	ACCESSION:AX297476
24	12.8	45.7	17	1	AX688609	ACCESSION:AX688609
25	12.8	45.7	17	1	E32811	ACCESSION:E32811
26	12.4	44.3	17	1	AX688601	ACCESSION:AX688601
27	12.4	44.3	18	1	AX711184	ACCESSION:AX711184
28	12.4	44.3	19	1	AR016655	ACCESSION:AR016655
29	12.4	44.3	19	1	AX110278	ACCESSION:AX110278
30	12.2	43.6	17	1	AX419338	ACCESSION:AX419338
31	12.2	43.6	17	1	AX688610	ACCESSION:AX688610
32	12.2	43.6	17	1	AX783828	ACCESSION:AX783828
33	12.2	43.6	17	1	AX783973	ACCESSION:AX783973

C	34	12.2	43.6	18	1	AR066781	ACCESSION:AR066781
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	36	12	42.9	17	1	AX688599	ACCESSION:AX688599
	37	12	42.9	17	1	AX688600	ACCESSION:AX688600
	38	11.8	42.1	16	1	BD246816	ACCESSION:BD246816
	39	11.8	42.1	16	1	AX026612	ACCESSION:AX026612
C	40	11.4	40.7	17	1	AX711182	ACCESSION:AX711182
	41	11.2	40.0	16	1	AR001333	ACCESSION:AR001333
	42	11.2	40.0	16	1	AR037513	ACCESSION:AR037513
	43	11.2	40.0	16	1	AR062793	ACCESSION:AR062793
	44	11.2	40.0	16	1	AR087871	ACCESSION:AR087871
	45	11.2	40.0	16	1	AR091341	ACCESSION:AR091341
	46	11.2	40.0	16	1	AR118047	ACCESSION:AR118047
	47	11.2	40.0	16	1	AR127765	ACCESSION:AR127765
	48	11.2	40.0	16	1	AR144933	ACCESSION:AR144933
	49	11.2	40.0	16	1	AR145934	ACCESSION:AR145934
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	51	11.2	40.0	17	1	BD259424	ACCESSION:BD259424
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	54	11.2	40.0	17	1	AX688611	ACCESSION:AX688611
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	57	11.2	40.0	17	1	AX783972	ACCESSION:AX783972
C	58	11.2	40.0	17	1	AX783974	ACCESSION:AX783974
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C	62	10.8	38.6	15	1	AR180569	ACCESSION:AR180569
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C	66	10	35.7	11	1	AX639206	ACCESSION:AX639206
	67	10	35.7	15	1	AR033531	ACCESSION:AR033531
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	74	9.8	35.0	14	1	AX8736	ACCESSION:AX8736
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	76	9.8	35.0	14	1	BD066249	ACCESSION:BD066249
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	79	9.8	35.0	15	1	BD263790	ACCESSION:BD263790
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C	85	9.4	33.6	11	1	AX627912	ACCESSION:AX627912
C	86	9.4	33.6	11	1	AX628430	ACCESSION:AX628430
C	87	9.4	33.6	11	1	AX628528	ACCESSION:AX628528
	88	9.4	33.6	12	1	AR19211	ACCESSION:AR19211
	89	9.4	33.6	12	1	AR362486	ACCESSION:AR362486
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C	91	9.2	32.9	14	1	AX42646	ACCESSION:AX42646
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C	95	9.2	32.9	14	1	AX711052	ACCESSION:AX711052
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120	8.4	30.0	10	1	BD166783	ACCESSION:BD166783	C 193	8	28.6	10	1	AX104933	ACCESSION:AX104933
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167	8.4	30.0	12	1	AR205443	ACCESSION:AR205443	C 240	7.8	27.9	11	1	AX625951	ACCESSION:AX625951
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262 7.8 27.9 11 1 AX627660
263 7.8 27.9 11 1 AX627965
264 7.8 27.9 11 1 AX628121
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267 7.8 27.9 11 1 AX629205
268 7.8 27.9 11 1 AX629571
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270 7.8 27.9 11 1 AX629882
271 7.8 27.9 11 1 AX630279
272 7.8 27.9 11 1 AX631061
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274 7.8 27.9 11 1 AX631751
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289 7.8 27.9 12 1 AX073604
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294 7.8 27.9 12 1 BP023278
295 7.8 27.9 25 1 AX690109
296 7.8 27.9 25 1 AX690110
297 7.8 27.9 25 1 AX690107
298 7.8 27.9 25 1 AX690108
299 7.8 27.9 25 1 AX690111
300 7.8 27.9 25 1 AX690112
301 7.6 27.1 10 1 AX096928
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## ALIGNMENTS

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RESULT 1
LOCUS AX690109 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 2841 from Patent EP1281758.
ACCESSION AX690109
VERSION AX690109.1 GI:29412967
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Shannon,M., Gu,Y. and Nguyen,C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
TITLE mdz12
JOURNAL Patent: EP 1281758-A 2841 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
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Db 1 GCCCTACGCTACAGGAGTCCAG 25

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DEFINITION Sequence 2842 from Patent EP1281758.
ACCESSION AX690110
VERSION AX690110.1 GI:29412968
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Shannon,M., Gu,Y. and Nguyen,C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
TITLE mdz12
JOURNAL Patent: EP 1281758-A 2842 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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Query Match 66.4%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 2.5;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DEFINITION Sequence 2839 from Patent EP1281758.
ACCESSION AX690107
VERSION AX690107.1 GI:29412965
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Shannon,M., Gu,Y. and Nguyen,C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
TITLE mdz12
JOURNAL Patent: EP 1281758-A 2839 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
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Query Match 65.0%; Score 18.2; DB 1; Length 25;
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FINITION	AX690108				
SSION	AX690108.1	GI:29412966			
(WORDS	Homo sapiens (human)				
JRCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	Shannon,M., Gu,Y. and Nguyen,C.T.				
AUTHORS	Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and				
TITLE	mdz12				
JOURNAL	Patent: EP 1281758-A 2840 05-FEB-2003;				
ATURES	Aeomica, Inc. (US)				
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SSION	AX690105.1	GI:29412963			
(WORDS	Homo sapiens (human)				
JRCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	Shannon,M., Gu,Y. and Nguyen,C.T.				
AUTHORS	Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and				
TITLE	mdz12				
JOURNAL	Patent: EP 1281758-A 2837 05-FEB-2003;				
ATURES	Aeomica, Inc. (US)				
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2 GGCCCTACGTTGCAGCGAGTGC 24					
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CUS	Sequence 2838 from Patent EPI281758.				
FINITION	AX690106				
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(WORDS	Homo sapiens (human)				
JRCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	Shannon,M., Gu,Y. and Nguyen,C.T.				
AUTHORS	Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and				
TITLE	mdz12				
JOURNAL	Patent: EP 1281758-A 2838 05-FEB-2003;				
ATURES	Aeomica, Inc. (US)				
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3 GGCCCTACGTTGCAGGGAGTCC 23					
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SULT 7	AX690107	25 bp	DNA	linear	PAT 31-MAR-2003
CUS	Sequence 2843 from Patent EPI281758.				
FINITION	AX690107				
SSION	AX690107.1	GI:29412969			
(WORDS	Homo sapiens (human)				
JRCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	Shannon,M., Gu,Y. and Nguyen,C.T.				
AUTHORS	Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and				
TITLE	mdz12				
JOURNAL	Patent: EP 1281758-A 2843 05-FEB-2003;				
ATURES	Aeomica, Inc. (US)				
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1 CCCTACGTTGCAGCGAGTGTGG 24					

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FEATURES
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        Patent: EP 1281758-A 1339 05-FEB-2003;
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QY
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DEFINITION
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ACCESSION
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VERSION
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KEYWORDS
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ORGANISM
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
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    AUTHORS
        Shannon,M., Gu,Y. and Nguyen,C.T.
    TITLE
        Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
        mdz12
    JOURNAL
        Patent: EP 1281758-A 1340 05-FEB-2003;
        Aeomica, Inc. (US)
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QY
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Db
    1 CTACGTGTGCGAGCAGT 17

RESULT 17
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LOCUS
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DEFINITION
    Sequence 1334 from Patent EP1281758.
ACCESSION
    AX688602
VERSION
    AX688602.1 GI:29411304
KEYWORDS
    Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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    AUTHORS
        Shannon,M., Gu,Y. and Nguyen,C.T.
    TITLE
        Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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    JOURNAL
        Patent: EP 1281758-A 1334 05-FEB-2003;
        Aeomica, Inc. (US)
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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b 3 GGCCTACGTGTCCA 17

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OCUS          AR058208          18 bp      DNA      linear      PAT 29-SEP-1999
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ACCESSION     AR058208
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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b 17 TGTACAGGAGTCCA 3

RESULT 19
R142361/c
OCUS          AR142361          18 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION    Sequence 6 from patent US 6174869.
ACCESSION     AR142361
VERSION       AR142361.1 GI:15102661
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 12 TGTACAGGAGTCCA 26
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b 17 TGTACAGGAGTCCA 3

RESULT 20
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OCUS          AX449606          20 bp      DNA      linear      PAT 03-JUL-2002
DEFINITION    Sequence 35 from Patent WO210216.
ACCESSION     AX449606
VERSION       AX449606.1 GI:21698215
KEYWORDS

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SOURCE          synthetic construct
ORGANISM         synthetic construct
REFERENCE        artificial sequences.
AUTHORS          Padigaru,M., Mezes,P., Mishra,V., Burgess,C., Casman,S.,
                  Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Gerlach,V.L.,
                  Macdougall,J.R. and Smithson,G.
TITLE            Proteins and nucleic acids encoding same
JOURNAL          Patent: WO 0210216-A 35 07-FEB-2002;
                  Curagen Corporation (US)
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Best Local Similarity 93.3%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 TACAGGGAGTCCAGG 28
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Db 17 TAGAGGGAGTCCAGG 3

RESULT 21
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LOCUS          BD088466          19 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    A method of arraying genome clone.
ACCESSION     BD088466
VERSION       BD088466.1 GI:22634076
KEYWORDS      JP 2001321190-A/710.
SOURCE        synthetic construct
ORGANISM       artificial sequences.
REFERENCE      Soeda,E.
AUTHORS        A method of arraying genome clone.
TITLE          Patent: JP 2001321190-A 710 20-NOV-2001;
JOURNAL        THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
COMMENT        GENOTECHS
                OS Artificial Sequence
                PN JP 2001321190-A/710
                PD 20-NOV-2001
                PF 12-MAR-2001 JP 2001068285
                PI EIICHI SOEDA
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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   |||||
Db 19 GTGTAGAGGTGCCAGG 2

RESULT 22
AB069243/c
LOCUS          AB069243          19 bp      DNA      linear      SYN 21-MAY-2003
DEFINITION    Synthetic construct DNA, reverse primer for human Srs-L07033 at

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1p36.
SESSION AB069243
SION AB069243.1 GI:15130047
WORDS
RCB synthetic construct
RGANISM synthetic construct
artificial sequences.
REFERENCE
1 Chen, Y.-Z., Hayashi, Y., Wu, J.-G., Takaoka, E., Maekawa, K.,
Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
Morihaishi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.,
and Soeda, E., A BAC-based STS-content map spanning a 35-Mb region of human
Chromosome 1p35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 19)
AUTHORS Horii, A
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES
Location/Qualifiers
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misc_feature 1..19
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sts-L07033 obtained from clones B7H21, B7I21, B13SE5,
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Human BAC library RPCI-11"
Query Match 47.1%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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19 GTGTAGGGGTGCCAGG 2

SULT 23
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FUNCTION Sequence 9238 from Patent WO0179549.
CDS AX297476
SION AX297476.1 GI:17059167
WORDS
URCE synthetic construct
RGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
Sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 9238 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Hypothetical Probe Sequence"
Query Match 47.1%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 30;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

10 CGTGTACAGGAGTCCAG 27
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Db 20 CGTGTGTAGGAGTCCGG 3

RESULT 24
AX688609
LOCUS AX688609 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1341 from Patent EP1281758.
ACCESSION AX688609
VERSION AX688609.1 GI:29411311
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 Shannon, M., Gu, Y. and Nguyen, C.T.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
Patent: EP 1281758-A 1341 05-FEB-2003;
Aemica, Inc. (US)
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 45.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TACGTGTACAGGAGT 23
||||| |||||||
1 TACGTGTGCAGCGAGT 16

Db 19 bp DNA linear PAT 31-JAN-2002
E32811
LOCUS E32811 19 bp DNA linear PAT 31-JAN-2002
DEFINITION Primer DNA and method for detecting mRNA encoding prostate
gland-specific antigen by using the same.
ACCESSION E32811
VERSION E32811.1 GI:18623941
KEYWORDS JP 2000069969-A/4.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Nakagawara, H.
TITLE Primer DNA and method for detecting mRNA encoding prostate
gland-specific antigen by using the same
JOURNAL Patent: JP 2000069969-A 4 07-MAR-2000;
HITACHI CHEMICAL CO LTD, KK NIHON IDENSHI KENKYUJO
COMMENT CS Unidentified
PD 07-MAR-2000
PF 28-AUG-1998 JP 1998243419
PR HIROKAZU NAKAGAWARA
PI C12N15/09, C12Q1/68, C12N15/00
PC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..19
/organism="Unidentified".
Location/Qualifiers
1..19
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 45.7%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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6 CCTACGTTACAGGA 21
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4 CCTGGTGTACAGGA 19

RESULT 26
ACUS AX688601 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1333 from Patent EP1281758.
ACCESSION AX688601
VERSION AX688601.1 GI:29411303
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1333 05-FEB-2003;
FEATURES
source
1. 17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 44.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 32;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

3 GGCCCTACGTGTAC 16
|||
4 GGCCCTACGTGTGC 17

RESULT 27
ACUS AX711184 18 bp DNA linear PAT 11-APR-2003
DEFINITION Sequence 484 from Patent EP1288296.
ACCESSION AX711184
VERSION AX711184.1 GI:29787565
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Draper, K.G., McSwiggen, J.A., Holecsek, J.J., Dudycz, L.W., Macejak, D.G. and Manone, J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 484 05-MAR-2003;
FEATURES
source
1. 18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Nucleic acid clone fragments"

Query Match 44.3%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 36;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CGGGCCCTACGTGT 14
|||
14 CGGGCCCGACGTGT 1

RESULT 28
ACUS AR016655 19 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 18 from patent US 5776762.
ACCESSION AR016655
VERSION AR016655.1 GI:3972932
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS North, M., Nishina, P., Noben-Trauth, K. and Naggert, J.
TITLE Obesity associated genes
JOURNAL Patent: US 5776762-A 18 07-JUL-1998;
FEATURES
source
1. 19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 44.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 41;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAGG 28
|||
DB 6 ACAGGAGACCAGG 19

RESULT 29
ACUS AR110278 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 30 from patent US 6114502.
ACCESSION AR110278
VERSION AR110278.1 GI:12826554
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS North, M., Nishina, P., Naggert, J. and Noben-Trauth, K.
TITLE Gene family associated with neurosensory defects
JOURNAL Patent: US 6114502-A 30 05-SEP-2000;
FEATURES
source
1. 19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 44.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 41;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAGG 28
|||
DB 6 ACAGGAGACCAGG 19

RESULT 30
ACUS AX419938 17 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 275 from Patent WO0198537.
ACCESSION AX419938
VERSION AX419938.1 GI:21524305
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Lyamichiev, V., Allawi, H., Dong, F., Meri, B.P. and Vener, I.T.
TITLE Nucleic acid accessible hybridization sites
JOURNAL Patent: WO 0198537-A 275 27-DEC-2001;
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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Query Match 43.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 36;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2 GGGCCCTAGTGTCACG 18
|||||
1 GGACCTATGTCACG 17

RESULT 33
AX783973/c
LOCUS AX783973 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2304 from Patent WO03050284.
ACCESSION AX783973
VERSION AX783973.1 GI:32951822
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Guo, J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2304 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 43.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 36;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTACGTGTACAGGGA 21
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DB 17 CCTACGTATTAAGAGA 1

RESULT 34
AR066781/c
LOCUS AR066781 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 129 from patent US 5851760.
ACCESSION AR066781
VERSION AR066781.1 GI:5998003
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Evans, G.A. and Smith, M.W.
TITLE Method for Generation of sequence sampled maps of complex genomes
JOURNAL Patent: US 5851760-A 129 22-DEC-1998;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 43.6%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGTCCAG 27
|||||
DB 18 GTGAAGAGGAGTCCGG 2

RESULT 35
AR083092
LOCUS AR083092 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 6 from patent US 5976803.
ACCESSION AR083092
VERSION AR083092.1 GI:10009882
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Meek, K.D.
TITLE Genetic test for equine severe combined immunodeficiency disease
JOURNAL Patent: US 5976803-A 6 02-NOV-1999;
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      /mol_type="unassigned DNA"
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  Best Local Similarity
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  Matches
    14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

12 TGTACAGGGAGTCCAGG 28
1 TCTACAGGGAGTCCAGG 17

RESULT 36
LOCUS
  AX688599
  DEFINITION
    Sequence 1331 from Patent EP1281758.
  ACCESSION
    AX688599
  VERSION
    AX688599.1 GI:29411301
  KEYWORDS
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1
    Shannon,M., Gu,Y. and Nguyen,C.T.
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    mdz12
  JOURNAL
    Patent: EP 1281758-A 1331 05-FEB-2003;
    Aeomica, Inc. (US)
  FEATURES
    source
      1..17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
  Query Match
    42.9%; Score 12; DB 1; Length 17;
  Best Local Similarity
    100.0%; Pred. No. 40;
  Matches
    12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 GGCCCTACGTGT 14
6 GGCCCTACGTGT 17

RESULT 37
LOCUS
  AX688600
  DEFINITION
    Sequence 1332 from Patent EP1281758.
  ACCESSION
    AX688600
  VERSION
    AX688600.1 GI:29411302
  KEYWORDS
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1
    Shannon,M., Gu,Y. and Nguyen,C.T.
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    mdz12
  JOURNAL
    Patent: EP 1281758-A 1332 05-FEB-2003;
    Aeomica, Inc. (US)
  FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
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  Best Local Similarity
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  Matches
    12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 GGCCCTACGTGT 14
5 GGCCCTACGTGT 16

RESULT 38
LOCUS
  BD246816
  DEFINITION
    Genotyping cytochrome expression.
  ACCESSION
    BD246816
  VERSION
    BD246816.1 GI:33056586
  KEYWORDS
    JP 2002533136-A/2.
  SOURCE
    synthetic construct
    synthetic construct
    artificial sequences.
  REFERENCE
    1 (bases 1 to 16)
    Paulussen,A.D.C. and Armstrong,M.
    Genotyping cytochrome expression
    Patent: JP 2002533136-A 2 08-OCT-2002;
    JANSSEN PHARMACEUTICA NV
  OS
    Artificial Sequence
  PN
    JP 2002533136-A/2
  PD
    08-OCT-2002
  PF
    22-DEC-1998 GB 9828619.8
  PI
    AIMEE DYMENE CATHERINE PAULUSSEN,MARTIN ARMSTRONG PC
    C12N15/09,C12Q1/02,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
    Description of Artificial Sequence:primer
  FH
    Key Location/Qualifiers
  FT
    source
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        /organism="Artificial Sequence".
        Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
  Query Match
    42.1%; Score 11.8; DB 1; Length 16;
  Best Local Similarity
    86.7%; Pred. No. 39;
  Matches
    13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

13 GTACAGGGAGTCCAG 27
2 GTACAGGGAGTCCAG 16

RESULT 39
LOCUS
  AX026612
  DEFINITION
    Sequence 2 from Patent WO0039332.
  ACCESSION
    AX026612
  VERSION
    AX026612.1 GI:10187786
  KEYWORDS
    synthetic construct
    synthetic construct
    artificial sequences.
  SOURCE
    Paulussen,A.D. and Armstrong,M.
  REFERENCE
    1
    Genotyping cytochrome expression
    Patent: WO 0039332-A 2 06-JUL-2000;
    JANSSEN PHARMACEUTICA NV (BE) ; PAULUSSEN AIMEE DYMENE CATHER (BE)
    ; ARMSTRONG MARTIN (GB)
  JOURNAL
    Location/Qualifiers
  FEATURES
    source
      1..16
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="primer"
  Query Match
    42.1%; Score 11.8; DB 1; Length 16;
  Best Local Similarity
    86.7%; Pred. No. 39;
  Matches
    13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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b 1 CGGTGCCAGGAGCC 16

RESULT 45  
LOCUS AR091341 16 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 23 from patent US 5994095.  
ACCESSION AR091341  
VERSION AR091341.1 GI:10018096  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Kamb,A.  
TITLE MTS2 gene  
JOURNAL Patent: US 5994095-A 23 30-NOV-1999;  
FEATURES  
source Location/Qualifiers  
1..16 /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred.No.54;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Y 10 CGGTACAGGGAGTCC 25  
|||||  
b 1 CGGTGCCAGGAGCC 16

RESULT 46  
LOCUS AR118047 16 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 23 from patent US 6140473.  
ACCESSION AR118047  
VERSION AR118047.1 GI:14098953  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Kamb,A.  
TITLE Antibodies specific for MTS2 Polypeptide  
JOURNAL Patent: US 6140473-A 23 31-OCT-2000;  
FEATURES  
source Location/Qualifiers  
1..16 /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred.No.54;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Y 10 CGGTACAGGGAGTCC 25  
|||||  
b 1 CGGTGCCAGGAGCC 16

RESULT 47  
LOCUS AR127766 16 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 23 from patent US 6180776.  
ACCESSION AR127766  
VERSION AR127766.1 GI:14114361  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Kamb,A.  
TITLE MTS2 gene  
JOURNAL Patent: US 6180776-A 23 30-JAN-2001;

FEATURES  
source Location/Qualifiers  
1..16 /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred.No.54;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Y 10 CGGTACAGGGAGTCC 25  
|||||  
b 1 CGGTGCCAGGAGCC 16

RESULT 48  
LOCUS AR144933 16 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 23 from patent US 6210949.  
ACCESSION AR144933  
VERSION AR144933.1 GI:15106800  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Stone,S., Jiang,P. and Kamb,A.  
TITLE Mouse MTS2 gene  
JOURNAL Patent: US 6210949-A 23 03-APR-2001;  
FEATURES  
source Location/Qualifiers  
1..16 /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred.No.54;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Y 10 CGGTACAGGGAGTCC 25  
|||||  
b 1 CGGTGCCAGGAGCC 16

RESULT 49  
LOCUS AR145934 16 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 23 from patent US 6218146.  
ACCESSION AR145934  
VERSION AR145934.1 GI:15109123  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Kamb,A.  
TITLE MTS2 gene  
JOURNAL Patent: US 6218146-A 23 17-APR-2001;  
FEATURES  
source Location/Qualifiers  
1..16 /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred.No.54;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Y 10 CGGTACAGGGAGTCC 25  
|||||  
b 1 CGGTGCCAGGAGCC 16

RESULT 50  
LOCUS I41167 16 bp DNA linear PAT 13-MAY-1997

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FINITION      Sequence 23 from patent US 5624819.
CESSION       I41167
RSION         I41167.1 GI:2081757
WORDS        Unknown.
URCE         Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 16)
AUTHORS      Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
TITLE        Germline mutations in the MTS gene
JOURNAL      Patent: US 5624819-A 23 29-APR-1997;
ATUES        Location/Qualifiers
            source
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

10 CGTGTACAGGAGTCC 25
1 CGTGTCCAGGAAGCC 16

SULT 51
259424
CUS          17 bp DNA linear PAT 17-JUL-2003
FINITION     Regulation of repressor genes using nucleic acid molecules.
CESSION      BD259424
RSION        BD259424.1 GI:33069194
WORDS       JP 2002541795-A/7217.
URCE        unidentified
ORGANISM     unclassified.
REFERENCE     1 (bases 1 to 17)
AUTHORS      Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE        Regulation of repressor genes using nucleic acid molecules
JOURNAL      Patent: JP 2002541795-A 7217 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT      OS Eukaryote
            PN TP 2002541795-A/7217
            PD 10-DEC-2002
            PF 11-APR-2000 JP 2000611654
            PR 12-APR-1999 US 60/129390
            PT LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
            C12R1:91),
            PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC A61K37/02,
            PC (C12N5/00,C12R1:91)
            CC Regulation of repressor genes using nucleic acid molecules FH
            Key source
            1..17
            Location/Qualifiers
            FT source
            1..17
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            /organism="Eukaryote".
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

7 CTACGTGTACAGGAG 22
1 CTACATGTACAGGAG 16

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RESULT 52
AX265559/c
LOCUS        AX265559 17 bp DNA linear PAT 26-OCT-2001
DEFINITION   Sequence 2950 from Patent WO0173002.
ACCESSION    AX265559
VERSION      AX265559.1 GI:16514358
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE     1
AUTHORS      Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE        Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
JOURNAL      Patent: WO 0173002-A 2950 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES     Location/Qualifiers
            source
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Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          9 ACGTGTACAGGAGTC 24
DB          17 ACTGTCCAGGAGGC 2

RESULT 53
AX265560
LOCUS        AX265560 17 bp DNA linear PAT 26-OCT-2001
DEFINITION   Sequence 2951 from Patent WO0173002.
ACCESSION    AX265560
VERSION      AX265560.1 GI:16514359
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE     1
AUTHORS      Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE        Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
JOURNAL      Patent: WO 0173002-A 2951 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES     Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          9 ACGTGTACAGGAGTC 24
DB          1 ACTGTCCAGGAGGC 16

RESULT 54
AX688611
LOCUS        AX688611 17 bp DNA linear PAT 31-MAR-2003
DEFINITION   Sequence 1343 from Patent EP1281758.
ACCESSION    AX688611
VERSION      AX688611.1 GI:29411313
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE        Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
              mdz12
JOURNAL      Patent: EP 1281758-A 1343 05-FEB-2003;
              Aescima, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 10 CGTGTCAGGAGTCC 25
      ||||| ||||| |||||
b 1 CGTGTCAGGAGTCC 16

RESULT 55
AX783827/c
LOCUS      AX783827 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2158 from Patent WO03050284.
ACCESSION  AX783827
VERSION     AX783827.1 GI:32951676
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Guo,J.
TITLE        Human prostate cancer candidate protein 1
JOURNAL      Patent: WO 03050284-A 2158 19-JUN-2003;
              Amersham Biosciences (SV) Corp. (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 13 GTACAGGAGTCCAGG 28
      ||||| ||||| |||||
b 17 GAAGAAGGAGTCAAG 2

RESULT 56
AX783829/c
LOCUS      AX783829 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2160 from Patent WO03050284.
ACCESSION  AX783829
VERSION     AX783829.1 GI:32951678
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Guo,J.
TITLE        Human prostate cancer candidate protein 1
JOURNAL      Patent: WO 03050284-A 2160 19-JUN-2003;
              Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 12 TGTACAGGAGTCCAG 27
      ||||| ||||| |||||
b 16 TGAAAAGGAGTCAAG 1

RESULT 57
AX783972/c
LOCUS      AX783972 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2303 from Patent WO03050284.
ACCESSION  AX783972
VERSION     AX783972.1 GI:32951821
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Guo,J.
TITLE        Human prostate cancer candidate protein 1
JOURNAL      Patent: WO 03050284-A 2303 19-JUN-2003;
              Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 6 CCTACGTGTACAGGGA 21
      ||||| ||||| |||||
b 17 CCTACGTATATAAGAGA 2

RESULT 58
AX783974/c
LOCUS      AX783974 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2305 from Patent WO03050284.
ACCESSION  AX783974
VERSION     AX783974.1 GI:32951823
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Guo,J.
TITLE        Human prostate cancer candidate protein 1
JOURNAL      Patent: WO 03050284-A 2305 19-JUN-2003;
              Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 5 CCTACGTGTACAGGG 20
      ||||| ||||| |||||
b 16 CCTACGTATATAAGAG 1

```

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RESULT 59
LOCUS AR033355 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 121 from patent US 5869253.
ACCESSION AR033355
VERSION AR033355.1 GI:5948960
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 121 09-FEB-1999;
FEATURES
LOCATION/Qualifiers
1..15
/mot_type="unassigned DNA"
/mot_type="unassigned DNA"

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

/
2 GGGCCCTACGTGTA 15
|||||
1 GGGCCCTCCGTGCA 14

/
3
2 GGGCCCTACGTGTA 15
|||||
1 GGGCCCTCCGTGCA 14

RESULT 60
LOCUS AR113177 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 121 from patent US 6132966.
ACCESSION AR113177
VERSION AR113177.1 GI:14093499
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 6132966-A 121 17-OCT-2000;
FEATURES
LOCATION/Qualifiers
1..15
/mot_type="unassigned DNA"
/mot_type="unassigned DNA"

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

/
2 GGGCCCTACGTGTA 15
|||||
1 GGGCCCTCCGTGCA 14

/
3
2 GGGCCCTACGTGTA 15
|||||
1 GGGCCCTCCGTGCA 14

RESULT 61
LOCUS AR033355 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 121 from patent US 5610054.
ACCESSION AR033355
VERSION AR033355.1 GI:2482648
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL Patent: US 5610054-A 121 11-MAR-1997;
FEATURES
LOCATION/Qualifiers
1..15
/mot_type="unassigned DNA"
/mot_type="unassigned DNA"

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

/
2 GGGCCCTACGTGTA 15
|||||
1 GGGCCCTCCGTGCA 14

/
3
2 GGGCCCTACGTGTA 15
|||||
1 GGGCCCTCCGTGCA 14

RESULT 62
LOCUS AR180569 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 637 from patent US 6333152.
ACCESSION AR180569
VERSION AR180569.1 GI:20222602
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 6333152-A 637 25-DEC-2001;
FEATURES
LOCATION/Qualifiers
1..15
/mot_type="unassigned DNA"
/mot_type="unassigned DNA"

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

/
2 GGGCCCTACGTGTA 15
|||||
1 GGGCCCTCCGTGCA 14

/
3
2 GGGCCCTACGTGTA 15
|||||
1 GGGCCCTCCGTGCA 14

RESULT 63
LOCUS BD207088 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD207088
VERSION BD207088.1 GI:33016858
KEYWORDS
SOURCE
ORGANISM unidentified.
REFERENCE
1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 678 08-MAY-2002;
COMMENT
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/678
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
hepatitis C virus infection.
PH Key Location/Qualifiers
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FT source 1..15
FT /organism='Hepatitis virus (hepatitis C FT
virus)',
FEATURES
source
1..15
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 2 GGGCCCTACGTGTA 15
| | | | |
b 1 GGGCCCTCCGTGCA 14

RESULT 64
ID065320/c
LOCUS BD065320 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065320
VERSION BD065320.1 GI:22610923
KEYWORDS JP 2001509017-A/256.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
1 (bases 1 to 10)
Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Characterization of the yeast transcriptome
JOURNAL Patent: JP 2001509017-A 256 10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/256
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Saccharomyces cerevisiae (yeast)',
FEATURES
source
1..10
Location/Qualifiers
/organism='Saccharomyces cerevisiae'
/mol_type='genomic DNA'
/db_xref='taxon:4932'

Query Match 35.7%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 14 TACAGGGAGT 23
| | | | |
b 10 TACAGGGAGT 1

RESULT 65
X470525/c
LOCUS AX470525 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 102 from Patent WO2053773.
ACCESSION AX470525
VERSION AX470525.1 GI:22205650
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Hofmann,K., Conradt,M. and Petersohn,D.
REFERENCE
AUTHORS

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TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 102 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'

Query Match 35.7%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 12 TGTACAGGGA 21
| | | | |
b 10 TGTACAGGGA 1

RESULT 66
AX629206/c
LOCUS AX629206 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6247 from Patent WO02053774.
ACCESSION AX629206
VERSION AX629206.1 GI:28457244
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6247 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'

Query Match 35.7%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 12 TGTACAGGGA 21
| | | | |
b 10 TGTACAGGGA 1

RESULT 67
AR033531
LOCUS AR033531 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 297 from patent US 5869253.
ACCESSION AR033531
VERSION AR033531.1 GI:5949136
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 297 09-FEB-1999;
FEATURES
source
1..15
Location/Qualifiers
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 19 GGAGTCCAGG 28

```

|||||  
3 GGAGTCCAGG 12

RESULT 68  
LOCUS AR113353 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 297 from patent US 6132966.  
ACCESSION AR113353  
VERSION AR113353.1 GI:14093675  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Draper K.G.  
TITLE Method and reagent for inhibiting hepatitis C virus replication  
JOURNAL Patent: US 6132966-A 297 17-OCT-2000;  
FEATURES Location/Qualifiers  
1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 35.7%; Score 10; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
19 GGAGTCCAGG 28  
|||||  
3 GGAGTCCAGG 12

RESULT 69  
LOCUS I38986 15 bp DNA linear PAT 13-MAY-1997  
DEFINITION Sequence 24 from patent US 5616488.  
ACCESSION I38986  
VERSION I38986.1 GI:2083466  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Sullivan, S., Draper, K.G., McSwiggen, J., and Stinchcomb, D.T.  
TITLE IL-5 targeted ribozymes  
JOURNAL Patent: US 5616488-A 24 01-APR-1997;  
FEATURES Location/Qualifiers  
1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 35.7%; Score 10; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
6 CCTACGTGTA 15  
|||||  
5 CCTACGTGTA 14

RESULT 70  
LOCUS I57760 15 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 297 from patent US 5610054.  
ACCESSION I57760  
VERSION I57760.1 GI:2482824  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Draper K.G.  
TITLE Enzymatic RNA molecule targeted against Hepatitis C virus

JOURNAL Patent: US 5610054-A 297 11-MAR-1997;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 35.7%; Score 10; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
19 GGAGTCCAGG 28  
|||||  
3 GGAGTCCAGG 12

RESULT 71  
LOCUS AX635280 15 bp RNA linear PAT 21-FEB-2003  
DEFINITION Sequence 2419 from Patent EP1260586.  
ACCESSION AX635280  
VERSION AX635280.1 GI:28470894  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Drenzo, A., Karpel, A., Draper, K.G., Kisch, K., Matulic-Adamic, J., McSwiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.  
TITLE Method and reagent for inhibiting the expression of disease related genes  
JOURNAL Patent: EP 1260586-A 2419 27-NOV-2002;  
FEATURES Location/Qualifiers  
1..15  
/organism="unidentified"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32644"

Query Match 35.7%; Score 10; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
6 CCTACGTGTA 15  
|||||  
5 CCTACGTGTA 14

RESULT 72  
LOCUS BD207264 15 bp RNA linear PAT 17-JUL-2003  
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.  
ACCESSION BD207264  
VERSION BD207264.1 GI:33017034  
KEYWORDS JP 2002512791-A/854.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Blatt, L., McSwiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.  
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection  
JOURNAL Patent: JP 2002512791-A 854 08-MAY-2002;  
COMMENT RIBOZYME PHARMACEUTICALS INC  
OS Hepatitis virus (hepatitis C virus)  
PN JP 2002512791-A/854  
PD 08-MAY-2002  
PF 26-APR-1999 JP 2000545991  
PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR  
25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI



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LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PI DENNIS MACEJAK
PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
PC A61K37/66,
PC C12N15/00,
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..15
FT virus),
FT Location/Qualifiers
FT 1..15
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 19 GGAGTCCAGG 28
|||||
b 3 GGAGTCCAGG 12

RESULT 73
LOCUS A42545 14 bp DNA linear PAT 06-MAR-1997
DEFINITION Sequence 61 from Patent WO9502051.
ACCESSION A42545
VERSION A42545.1 GI:2297994
KEYWORDS
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen, G., Schlingensiepen, R., Schlingensiepen, K. and Brysch, W.
TITLE A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
JOURNAL
COMMENT Patent: WO 9502051-A 61 19-JAN-1995;
BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
Other publication AU 7345694 950206.
FEATURES
source 1..14
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 35.0%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 10 CGGTACAGGAG 22
|||||
b 2 CGGTACAGGAG 14

RESULT 74
LOCUS A88736 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 884 from Patent WO9833904.
ACCESSION A88736
VERSION A88736.1 GI:6737306
KEYWORDS
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 14)

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Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
Patent: WO 9833904-A 884 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source 1..14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 35.0%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 10 CGGTACAGGAG 22
|||||
b 2 CGGTACAGGAG 14

RESULT 75
LOCUS AR253087/c 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 38 from patent US 6479242.
ACCESSION AR253087
VERSION AR253087.1 GI:27301448
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Guo, B. and Sun, X.
TITLE Method for genotyping of single nucleotide polymorphism
JOURNAL Patent: US 6479242-A 38 12-NOV-2002;
FEATURES
source 1..14
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.0%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 12 TGTACAGGAGTC 24
|||||
b 14 TGGCAGGAGTC 2

RESULT 76
LOCUS BD066249 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066249
VERSION BD066249.1 GI:22611852
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen, K. H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 200151000-A 884 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 200151000-A/884
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
PC C12N15/11, C07H21/04, A61K31/70
CC An antisense oligonucleotide preparation method FH Key
SOURCE Location/Qualifiers
FT source 1..14
/organism="Unknown".

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FEATURES             Location/Qualifiers
     source
     1..14
     /organism="unidentified"
     /mol_type="genomic DNA"
     /db_xref="taxon:32644"

Query Match
Best Local Similarity 35.0%; Score 9.8; DB 1; Length 14;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

10 CGTCTACAGGAG 22
2 CGTCTACAGAG 14

RESULT 77
LOCUS             15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION
Adeno-associated virus-delivered ribozyme compositions and methods
of use.
ACCESSION
BD263790
VERSION
BD263790.1 GI:33073558
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and
Burger,C.
TITLE
Adeno-associated virus-delivered ribozyme compositions and methods
of use
JOURNAL
Patent: JP 2002542805-A 12 17-DEC-2002;
UNIVERSITY OF FLORIDA
COMMENT
OS Artificial Sequence
PN JP 2002542805-A/12
PD 17-DEC-2002
PF 28-APR-2000 JP 2000615402
PR 30-APR-1999 US 60/131942
PI ALFRED S LEWIN,NICHOLAS MUZYCZKA,WILLIAM W HAUSWIRTH PI
,CHRISTIAN TESCHENDORF,
PI CORINNA BURGER
PC C12N15/09,A01K67/027,C12N9/00,C12Q1/68,C12N15/00 CC
Description of Artificial Sequence: SYNTHETIC PEPTIDE PH Key
FEATURES             Location/Qualifiers
     source
     1..15
     /organism="synthetic construct"
     /mol_type="genomic RNA"
     /db_xref="taxon:32630"

Query Match
Best Local Similarity 35.0%; Score 9.8; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 GGCCTACGTGTA 15
2 GCCCTACGTATA 14

RESULT 78
LOCUS             15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION
Sequence 115 from patent US 6132966.
ACCESSION
AR113171
VERSION
AR113171.1 GI:14093493
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Draper,K.G.
TITLE
Method and reagent for inhibiting hepatitis C virus replication
JOURNAL
Patent: US 6132966-A 115 17-OCT-2000;
FEATURES             Location/Qualifiers
     source
     1..15
     /organism="unknown"
     /mol_type="unassigned DNA"

Query Match
Best Local Similarity 35.0%; Score 9.8; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 GGCCTACGTGTA 15
2 GCCCTACGTATA 14

RESULT 79
LOCUS             15 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION
Sequence 115 from patent US 5610054.
ACCESSION
I57578
VERSION
I57578.1 GI:2482642
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Draper,K.G.
TITLE
Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL
Patent: US 5610054-A 115 11-MAR-1997;
FEATURES             Location/Qualifiers
     source
     1..15
     /organism="unknown"
     /mol_type="unassigned DNA"

Query Match
Best Local Similarity 35.0%; Score 9.8; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 GGCCTACGTGTA 15
2 GCCCTACGTATA 14

RESULT 81

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X048276
ACUUS AX048276 15 bp RNA linear PAT 15-DEC-2000
DEFINITION Sequence 12 from Patent WO0066780.
ACCESSION AX048276
VERSION AX048276.1 GI:11877041
KEYWORDS synthetic construct
ORGANISM synthetic construct
SOURCE artificial sequences.
REFERENCE 1
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and
Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods
of use
JOURNAL Patent: WO 0066780-A 12 09-NOV-2000;
UNIVERSITY OF FLORIDA (US)
FEATURES
source
1. .15
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32830"
/notes="SYNTHETIC PEPTIDE"
Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Y 16 CAGGAGTCCAGG 28
| | | | |
b 1 CAGACAGTCCAGG 13

RESULT 82
ACUUS AX362585 15 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 19 from Patent WO0208425.
ACCESSION AX362585
VERSION AX362585.1 GI:18694729
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Finkel,K. and Koshy,B.
TITLE Haplotypes of the adrb3 gene
JOURNAL Patent: WO 0208425-A 19 31-JAN-2002;
GENAissance Pharmaceuticals, Inc. (US)
FEATURES
source
1. .15
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Y 11 GTGTACAGGAGT 23
| | | | |
b 13 GTGCCAGGAGT 1

RESULT 83
ACUUS BD207082 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD207082
VERSION BD207082.1 GI:33016852
KEYWORDS JP 2002512791-A/672.
ORGANISM unidentified
SOURCE unidentified

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unclassified.
1 (bases 1 to 15)
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 672 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/672
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
FH Key Location/Qualifiers
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virus),/organism="Hepatitis virus (hepatitis C FT
Location/Qualifiers
1. .15
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Y 3 GCCCTACGTGTA 15
| | | | |
b 2 GCCCTACGTATA 14

RESULT 84
ACUUS AX625951 11 bp DNA linear PAT 21-FEB-2003
LOCUS Sequence 2392 from Patent WO02053774.
DEFINITION AX625951
ACCESSION AX625951
VERSION AX625951.1 GI:28453989
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2392 11-JUL-2002;
HENKEL KOMMANDITGESSELLSCHAFT AUF AKTIEN (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 12 TGTACAGGAG 22
| | | | |
b 11 TGTACAGGAG 1

RESULT 85

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627912/c
CUS AX627912 11 bp DNA linear PAT 21-FEB-2003
SEQUENCE Sequence 4953 from Patent WO02053774.
CESSION AX627912
SION AX627912.1 GI:28455950
WORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 4953 11-JUL-2002; (DE)
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 18 GGGAGTCCAGG 28
b 11 GGGATTCAGG 1
RESULT 86
CUS AX628430 11 bp DNA linear PAT 21-FEB-2003
SEQUENCE Sequence 5471 from Patent WO02053774.
CESSION AX628430
SION AX628430.1 GI:28456468
WORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 5471 11-JUL-2002; (DE)
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 18 GGGAGTCCAGG 28
b 11 GGGATTCAGG 1
RESULT 87
CUS AX628528 11 bp DNA linear PAT 21-FEB-2003
SEQUENCE Sequence 5569 from Patent WO02053774.
CESSION AX628528
SION AX628528.1 GI:28456566
WORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 5569 11-JUL-2002; (DE)
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 18 GGGAGTCCAGG 28
b 11 GGGATTCAGG 1
RESULT 88
CUS AX628486 12 bp DNA linear PAT 03-SEP-2003
SEQUENCE Sequence 2 from patent US 5174962.
CESSION AR362486
SION AR362486.1 GI:34422687
WORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Nallur,G.N. and Hu,X.
TITLE Methods and devices for measuring differential gene expression
JOURNAL Patent: US 6355423-A 67 12-WAR-2002;
FEATURES Location/Qualifiers
source
1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 6 CCTACGCTGATC 16
b 2 CCTACCTGTATC 12
RESULT 89
CUS AR362486 12 bp DNA linear PAT 03-SEP-2003
SEQUENCE Sequence 2 from patent US 5174962.
CESSION AR362486
SION AR362486.1 GI:34422687
WORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Brennan,T.M.
TITLE Apparatus for determining DNA sequences by mass spectrometry
JOURNAL Patent: US 5174962-A 2 29-DEC-1992;
FEATURES Location/Qualifiers
source
1..12
/organism="unknown"
/mol_type="genomic DNA"
Query Match 33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 9 ACGTGTACAGG 19
b 1 ACGTGTACAGG 11

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AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5569 11-JUL-2002;
FEATURES Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 12 TGTACAGGGAG 22
b 11 TGTACAGGGTG 1
RESULT 88
CUS AR199211 12 bp DNA linear PAT 20-APR-2002
SEQUENCE Sequence 67 from patent US 6355423.
CESSION AR199211
SION AR199211.1 GI:20249285
WORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Nallur,G.N. and Hu,X.
TITLE Methods and devices for measuring differential gene expression
JOURNAL Patent: US 6355423-A 67 12-WAR-2002;
FEATURES Location/Qualifiers
source
1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 6 CCTACGCTGATC 16
b 2 CCTACCTGTATC 12
RESULT 89
CUS AR362486 12 bp DNA linear PAT 03-SEP-2003
SEQUENCE Sequence 2 from patent US 5174962.
CESSION AR362486
SION AR362486.1 GI:34422687
WORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Brennan,T.M.
TITLE Apparatus for determining DNA sequences by mass spectrometry
JOURNAL Patent: US 5174962-A 2 29-DEC-1992;
FEATURES Location/Qualifiers
source
1..12
/organism="unknown"
/mol_type="genomic DNA"
Query Match 33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 9 ACGTGTACAGG 19
b 1 ACGTGTACAGG 11

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RESULT 90
R362486/c
OCUS
DEFINITION Sequence 2 from patent US 5174962.
ACCESSION AR362486
VERSION AR362486.1 GI:34422687
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Brennan,T.M.
TITLE Apparatus for determining DNA sequences by mass spectrometry
JOURNAL Patent: US 5174962-A 2 29-DEC-1992;
FEATURES
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            /organism="unknown"
            /mol_type="genomic DNA"
Query Match 33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 9 ACCTGTACAGG 19
b 12 ACGTGTACAGG 2
RESULT 91
A42646/c
OCUS
DEFINITION Sequence 164 from Patent WO9502051.
ACCESSION A42646
VERSION A42646.1 GI:2298095
KEYWORDS
SOURCE
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and Brysch,W.
TITLE A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
JOURNAL Patent: WO 9502051-A 164 19-JAN-1995;
COMMENT BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
FEATURES
    Location/Qualifiers
        1..14
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
Query Match 32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Y 6 CCTACGTCGTACAGG 19
b 14 CCTCTGTATACAGG 1
RESULT 92
A8835/c
OCUS
DEFINITION Sequence 983 from Patent WO9833904.
ACCESSION A8835
VERSION A8835.1 GI:6737405
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

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unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 983 06-AUG-1998; (DE)
FEATURES
    Location/Qualifiers
        1..14
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
Query Match 32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Y 6 CCTACGTCGTACAGG 19
b 14 CCTCTGTATACAGG 1
RESULT 93
AR024070/c
LOCUS
DEFINITION Sequence 20 from patent US 5795778.
ACCESSION AR024070
VERSION AR024070.1 GI:3977364
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting herpes simplex virus replication
JOURNAL Patent: US 5795778-A 20 18-AUG-1998;
FEATURES
    Location/Qualifiers
        1..14
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Y 10 CGTGTACAGGGAGT 23
b 14 CGTGATCAGGGCGT 1
RESULT 94
AR224289/c
LOCUS
DEFINITION Sequence 20 from patent US 6440719.
ACCESSION AR224289
VERSION AR224289.1 GI:23333066
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting herpes simplex virus replication
JOURNAL Patent: US 6440719-A 20 27-AUG-2002;
FEATURES
    Location/Qualifiers
        1..14
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match 32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Y 10 CGTGTACAGGGAGT 23

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PC	C12N15/09,C12N5/10,C12N7/00,C12N9/22/(C12N5/10,C12R1:91), PC
PC	C12N15/00, (C12N5/00,C12R1:91)
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FT	source
FEATURES	
source	
Query Match	32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity	78.6%; Pred. No. 1.2e+02;
Matches	11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	10 CGTGATCAGGCGT 23
Db	14 CGTGATCAGGCGT 1
RESULT 97	
BD001603	14 bp RNA linear PAT 31-JAN-2002
LOCUS	Method and reagent for inhibiting viral replication.
DEFINITION	
ACCESSION	BD001603.1 GI:18626162
VERSION	JP 2000342286-A/334.
KEYWORDS	synthetic construct
SOURCE	artificial sequences
ORGANISM	1 (bases 1 to 14)
REFERENCE	Draper,K.G., Dadykzt,L.W., Macswigen,J.A., Maysejak,D.G.,
AUTHORS	Holesek,J.J. and Mamone,A.J.
TITLE	Method and reagent for inhibiting viral replication
JOURNAL	Patent: JP 2000342286-A 334 12-DEC-2000;
COMMENT	RIBOZYME PHARMACEUTICALS INC
	OS Artificial Sequence
	PN JP 2000342286-A/334
	PD 12-DEC-2000
	PF 01-MAY-2000 JP 2000132651
	PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
	14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
	14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
	14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
	14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
	14-MAY-1992 US 07/882922,14-MAY-1992 US 07/882923 PR
	14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
	14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884333 PR
	14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
	31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
	26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
	15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
	07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PR
	KENNETH G DRAPER,LEC W DADYKZT,JAMES A MACSWIGEN, PI DENNIS G
	MAYSEJAK,
	PI JAMES J HOLESEK,ANTHONY J MAMONE
	PC C12N15/09,C12N5/10,C12N7/00/(A61K38/43,A61K39/125,A61K39/13,
	PC A61K39/135,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
	PC A61P1/16,
	PC A61P3/14,A61P3/16,A61P3/18,A61P3/22,A61P35/02,C12Q1/68, PC
	(C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
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FT	1. .14 /organism='Artificial Sequence'
FT	source
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source	
Query Match	32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity	78.6%; Pred. No. 1.2e+02;
Matches	11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	10 CGTGATCAGGCGT 23
Db	14 CGTGATCAGGCGT 1
RESULT 96	
BD001174	14 bp RNA linear PAT 31-JAN-2002
LOCUS	Method and reagent for inhibiting viral replication.
DEFINITION	
ACCESSION	BD001174.1 GI:18625733
VERSION	JP 2000342285-A/334.
KEYWORDS	synthetic construct
SOURCE	artificial sequences
ORGANISM	1 (bases 1 to 14)
REFERENCE	Draper,K.G., Dadykzt,L.W., Macswigen,J.A., Maysejak,D.G.,
AUTHORS	Holesek,J.J. and Mamone,A.J.
TITLE	Method and reagent for inhibiting viral replication
JOURNAL	Patent: JP 2000342285-A 334 12-DEC-2000;
COMMENT	RIBOZYME PHARMACEUTICALS INC
	OS Artificial Sequence
	PN JP 2000342285-A/334
	PD 12-DEC-2000
	PF 01-MAY-2000 JP 2000132616
	PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
	14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
	14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
	14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
	14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
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	14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
	14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
	14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
	14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
	31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
	26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
	15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
	07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PR
	KENNETH G DRAPER,LEC W DADYKZT,JAMES A MACSWIGEN, PI DENNIS G
	MAYSEJAK,
	PI JAMES J HOLESEK,ANTHONY J MAMONE

/mol\_type="genomic RNA"  
/db\_xref="taxon:32630"

Query Match 32.9%; Score 9.2; DB 1; Length 14;  
Best Local Similarity 78.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Y 10 CGTGACAGGAGCT 23  
b 14 CGTGATCAGGCGT 1

RESULT 98  
ID066348/c  
LOCUS BD066348 14 bp DNA linear PAT 27-AUG-2002  
DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD066348  
VERSION BD066348.1 GI:22611951  
KEYWORDS JP 2001511000-A/983.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Schlingensiefen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 983 07-AUG-2001;  
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
OS Unknown  
PN JP 2001511000-A/983  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEFEN,WOLFGANG BRYSCH  
PC C12N15/11,C07H21/04,A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
Location/Qualifiers  
FT source 1..14  
FEATURES  
source Location/Qualifiers  
1..14  
/organism="Unknown".

Query Match 32.9%; Score 9.2; DB 1; Length 14;  
Best Local Similarity 78.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 6 CCTACGTGTACAGG 19  
b 14 CCTCTGTATACAGG 1  
RESULT 99  
AX152114  
LOCUS AX152114 10 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 29 from Patent WO0138577.  
ACCESSION AX152114  
VERSION AX152114.1 GI:14533765  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1  
Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
Human transcripomes  
Patent: WO 0138577-A 29 31-MAY-2001;  
The Johns Hopkins University (US)  
Location/Qualifiers  
1..10  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"

Query Match 32.1%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 8 TAGCTGTAC 16  
b 11 TAGCTGTAC 3  
RESULT 100  
AX626581/c  
LOCUS AX626581 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3622 from Patent WO02053774.  
ACCESSION AX626581  
VERSION AX626581.1 GI:28454619  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1  
Petersohn,D., Conradt,M. and Hofmann,K.  
Method for determining homeostasis of the skin  
Patent: WO 02053774-A 5502 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

Query Match 32.1%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 20 GAGTCCAGG 28  
b 2 GAGTCCAGG 10

RESULT 100  
AX626581/c  
LOCUS AX626581 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3622 from Patent WO02053774.  
ACCESSION AX626581  
VERSION AX626581.1 GI:28454619  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1  
Petersohn,D., Conradt,M. and Hofmann,K.  
Method for determining homeostasis of the skin  
Patent: WO 02053774-A 3622 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 32.1%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 19 GGAGTCCAG 27  
b 9 GGAGTCCAG 1  
RESULT 101  
AX628461/c  
LOCUS AX628461 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5502 from Patent WO02053774.  
ACCESSION AX628461  
VERSION AX628461.1 GI:28456499  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1  
Petersohn,D., Conradt,M. and Hofmann,K.  
Method for determining homeostasis of the skin  
Patent: WO 02053774-A 5502 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 32.1%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 8 TAGCTGTAC 16  
b 11 TAGCTGTAC 3  
RESULT 101  
AX628461/c  
LOCUS AX628461 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5502 from Patent WO02053774.  
ACCESSION AX628461  
VERSION AX628461.1 GI:28456499  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1  
Petersohn,D., Conradt,M. and Hofmann,K.  
Method for determining homeostasis of the skin  
Patent: WO 02053774-A 5502 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

SULT 102  
7646/c

CUS A47646 12 bp DNA linear PAT 07-MAR-1997  
FINITION Sequence 6 from Patent EP0692535.  
SESSION A47646  
RSTON A47646.1 GI:2301587

WORDS  
UNCE unidentified  
ORGANISM unidentified

REFERENCE 1 (bases 1 to 12)  
AUTHORS Colote,S. and Pirotzky,E.  
TITLE Oligonucleotides to inhibit the role of isoprenyl protein  
JOURNAL transferases

MENT Patent: EP 0692535-A 6 17-JAN-1996;

SOD CONSEILS RECH APPLIC (FR)

Other publication CN 1124142 960612

Other publication CZ 9501688 960515

Other publication BR 9503015 960604

Other publication NZ 722398 960426

Other publication HU 72133 960328

Other publication JP 8051985 960227

Other publication FR 2721930 960105

Other publication FR 2721827 960105

Other publication FI 953170 951230

Other publication SE 9502259 951230

Other publication PT 309384 960108

Other publication AU 952601 960102

Other publication AU 2329995 960111

Other publication CA 2152333 951230

Other publication GB 2290791 960110.

Location/Qualifiers

1. .12

/organism="unidentified"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32644"

Query Match 32.1%; Score 9; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

13 GTACAGGGA 21

12 GTACAGGGA 4

SULT 103  
027864/c

CUS AR027864 12 bp DNA linear PAT 29-SEP-1999  
FINITION Sequence 6 from patent US 5856461.  
SESSION AR027864  
RSTON AR027864.1 GI:5938684

WORDS Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)

AUTHORS Colote,S. and Pirotzky,E.

TITLE Oligonucleotides to inhibit the expression of isoprenyl protein

JOURNAL transferases

Patent: US 5856461-A 6 05-JAN-1999;

Location/Qualifiers

1. .12

/organism="unknown"

/mol\_type="unassigned DNA"

source

Query Match 32.1%; Score 9; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

13 GTACAGGGA 21

12 GTACAGGGA 4

RESULT 104  
BD259424/c

LOCUS Regulation of repressor genes using nucleic acid molecules.  
DEFINITION Regulation of repressor genes using nucleic acid molecules.  
ACCESSION BD259424  
VERSION BD259424.1 GI:33069194  
KEYWORDS JP 2002541795-A/7217.  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE 1 (bases 1 to 17)

AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.

TITLE Regulation of repressor genes using nucleic acid molecules

JOURNAL Patent: JP 2002541795-A 7217 10-DEC-2002;

COMMENT RIBOZYME PHARMACEUTICALS INC

OS Eukaryote

PN JP 2002541795-A/7217

PD 10-DEC-2002

PF 11-APR-2000 JP 2000611654

PR 12-APR-1999 US 60/129390

PI LAWRENCE BLATT MICHAEL ZWICK PAMELA PAVCO JAMES MCSWIGGEN PC

C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC

C12P21/02,

PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1/91),(C12P21/02, PC

C12R1/91),

PC (C12P21/02,C12R1/91),(C12P21/02,C12R1/91),C12N15/00,C12N5/00,

PC A61K37/02,

PC (C12N5/00,C12R1/91)

CC Regulation of repressor genes using nucleic acid molecules FH

Key source 1. .17

FT Location/Qualifiers

FT 1. .17

Location/Qualifiers

/organism="Eukaryote".

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/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

Query Match 32.1%; Score 9; DB 1; Length 17;

Best Local Similarity 70.6%; Pred. No. 1.8e+02;

Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

6 CCTACGTGTACAGGAG 22

17 CCTCCTGGTACATGTAG 1

Qy

Db

RESULT 105

AR199211/c

LOCUS Sequence 67 from patent US 6355423.

DEFINITION

ACCESSION AR199211

VERSION AR199211.1 GI:20249285

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)

AUTHORS Rothberg,J.Marc., Nallur,G.N. and Hu.X.

TITLE Methods and devices for measuring differential gene expression

JOURNAL Patent: US 6355423-A 67 12-MAR-2002;

Location/Qualifiers

1. .12

/organism="unknown"

/mol\_type="unassigned DNA"

source

Query Match 31.4%; Score 8.8; DB 1; Length 12;

Best Local Similarity 83.3%; Pred. No. 1e+02;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



Y 13 GTACAGGAGTC 24  
 |||||  
 b 12 GTACAGTAGGC 1

## RESULT 106

97287  
 OCUS A97287 12 bp DNA linear PAT 26-JAN-2000  
 DEFINITION Sequence 4 from Patent WO9918197.  
 CCESSION A97287  
 ERSION A97287.1 GI:6780670  
 EYNORDS  
 ORGANISM

REFERENCE  
 1 (bases 1 to 12)

unclassified

unclassified

unclassified

unclassified

Yaspo,M. and Lehrach,H.

NUCLEIC ACID MOLECULE ENCODING A (POLY)PEPTIDE CO-SEGREGATING IN

MUTATED FORM WITH AUTOIMMUNE POLYENDOCRINOPATHY CANDIDIASIS

ECTODERMAL DYSTROPHY (APECED)

Patent: WO 9918197-A 4 15-APR-1999;

MAX PLANCK GESLLSCHAFT (DE); YASPO MARIE LAURE (DE)

FEATURES

source

1..12

/organism="unidentified"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32644"

Query Match 31.4%; Score 8.8; DB 1; Length 12;

Best Local Similarity 83.3%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 15 ACAGGAGTGCCA 26

|||||

b 1 ACAGGAGGCCA 12

## RESULT 107

R167847/c  
 OCUS AR167847 12 bp DNA linear PAT 17-DEC-2001  
 DEFINITION Sequence 211 from patent US 6287769.  
 CCESSION AR167847  
 ERSION AR167847.1 GI:17903654  
 EYNORDS  
 ORGANISM

REFERENCE  
 1 (bases 1 to 12)

unclassified

unclassified

unclassified

unclassified

Inoue,T.

Method of amplifying DNA fragment, apparatus for amplifying DNA

fragment, method of assaying microorganisms, method of analyzing

microorganisms and method of assaying contaminant

Patent: US 6287769-A 211 11-SEP-2001;

FEATURES

source

1..12

/organism="unknown"

/mol\_type="unassigned DNA"

Query Match 31.4%; Score 8.8; DB 1; Length 12;

Best Local Similarity 83.3%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 5 CCTACCGTGTCAC 16

|||||

b 12 CCATACGTGCAC 1

## RESULT 108

129731/c  
 OCUS E29731 12 bp DNA linear PAT 18-JUN-2001  
 DEFINITION Method for amplifying DNA fragment, method for estimating state of  
 microorganism existing and method for estimating state of waste.  
 CCESSION E29731

E29731.1 GI:13021234  
 JP 1999276176-A/211.  
 unclassified  
 unclassified

REFERENCE  
 1 (bases 1 to 12)

unclassified

unclassified

unclassified

Koichi, I.

Method for amplifying DNA fragment, method for estimating state of

microorganism existing and method for estimating state of waste

Patent: JP 1999276176-A 211 12-OCT-1999;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE

FORESTRY AND FISHERIES

OS Unidentified

PN JP 1999276176-A/211

PD 12-OCT-1999

PF 31-MAR-1998 JP 1998087652

PR KOICHI INOUE

PC C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC

Strandedness: Single;

FT Key Location/Qualifiers

FT source 1..12

FT Location/Qualifiers

FT /organism="Unidentified".

source

1..12

/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

Query Match 31.4%; Score 8.8; DB 1; Length 12;

Best Local Similarity 83.3%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 5 CCTACGTGTAC 16

|||||

b 12 CCATACGTGCAC 1

## RESULT 109

E38837/c  
 LOCUS E38837 12 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Method and device for amplifying DNA fragment.  
 CCESSION E38837  
 ERSION E38837.1 GI:18621499  
 EYNORDS JP 2000270867-A/211.  
 ORGANISM

REFERENCE  
 1 (bases 1 to 12)

unclassified

unclassified

unclassified

Inoue,K.

Method and device for amplifying DNA fragment

Patent: JP 2000270867-A 211 03-OCT-2000;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE

FORESTRY AND FISHERIES

OS Unidentified

PN JP 2000270867-A/211

PD 03-OCT-2000

PF 19-MAR-1999 JP 1999076844

PR KOICHI INOUE

PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00

Strandedness: Single;

CC Topology: Linear;

CC Key Location/Qualifiers

FT source 1..12

FT Location/Qualifiers

FT /organism="Unidentified".

source

1..12

/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

Query Match 31.4%; Score 8.8; DB 1; Length 12;



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ERSON      AR178839.1  GI:20219977
EYWORDS
ORCE
ORGANISM
REFERENCE
AUTHORS      Bennett,C.Frank. and Vickers,T.A.
TITLE      Oligonucleotide compositions and methods for the modulation of the
            expression of B7 protein
JOURNAL      Patent: US 6319905-A 85 20-NOV-2001;
FEATURES      Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y      13  GTACAGGGAG 22
b      10  GTACAGGGAG 1

RESULT 115
54652/c
CCUS      E54652      10 bp  DNA  linear  PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.
CESSION    E54652
JOURNAL    E54652.1  GI:22556135
EYWORDS    JP 2001211883-A/4.
ORCE      Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human normal liver cell expression genes
JOURNAL    Patent: JP 2001211883-A 4 07-AUG-2001;
FEATURES    SCIENCE & TECH AGENCY
            OS Homo sapiens (human)
            PN JP 2001211883-A/4
            PD 07-AUG-2001
            PF 31-JAN-2000 JP 2000023170
            PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
            YAMASHITA
            CC C12N15/09,C07K16/18,C12P21/02,C12N15/00
            FH Key Location/Qualifiers.
            source
            1..10
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y      18  GGGAGTCCAG 27
b      10  GGGAGGCCAG 1

RESULT 116
R336839
CCUS      AR336839      10 bp  DNA  linear  PAT 17-AUG-2003
DEFINITION Sequence 14 from patent US 6566130.
CESSION    AR336839
JOURNAL    AR336839
EYWORDS    AR336839.1  GI:33722689
ORCE      Unknown.
ORGANISM   Unknown.

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Unclassified.
1 (bases 1 to 10)
AUTHORS      Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
TITLE      Androgen-regulated Gene expressed in prostate tissue
JOURNAL      Patent: US 6566130-A 14 20-MAY-2003;
FEATURES      Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y      13  GTACAGGGAG 22
b      1  GTGCAGGGAG 10

RESULT 117
AX113024/c
LOCUS      AX113024      10 bp  DNA  linear  PAT 01-MAY-2001
DEFINITION Sequence 71 from Patent WO0127267.
CESSION    AX113024
JOURNAL    AX113024
EYWORDS    AX113024.1  GI:13939459
ORCE      Mus sp.
ORGANISM   Mus sp.
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS    Adams,E., Waldmann,H., Cobbold,S. and Zelenika,D.
TITLE      Genes differentially expressed in tr1 cells and their use in the
            manufacture of immunoregulatory compositions
JOURNAL    Patent: WO 0127267-A 71 19-APR-2001;
            ISIS INNOVATION LIMITED (GB)
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="Mus sp."
            /mol_type="unassigned DNA"
            /db_xref="taxon:10095"
Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y      12  TGTACAGGGA 21
b      10  TGTACGGGGA 1

RESULT 118
AX153342/c
LOCUS      AX153342      10 bp  DNA  linear  PAT 22-JUN-2001
DEFINITION Sequence 1257 from Patent WO0138577.
CESSION    AX153342
JOURNAL    AX153342.1  GI:14534993
EYWORDS    Homo sapiens (human)
ORCE      Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcripts
JOURNAL    Patent: WO 0138577-A 1257 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

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Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

12 TGTACAGGGA 21
|||||
10 TGTACGGGGA 1

RESULT 119
LOCUS      AX377356          10 bp      DNA      linear      PAT 18-MAR-2002
DEFINITION Sequence 20 from Patent WO0212499.
ACCESSION  AX377356
VERSION     AX377356.1 GI:19573642
KEYWORDS    Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 10)
AUTHORS      Kliem,S.E., Koshy,B. and Lanz,E.M.
TITLE        Haplotypes of the ntf3 gene
JOURNAL      Patent: WO 0212499-A 20 14-FEB-2002;
              Genasance Pharmaceuticals, Inc. (US)
COMMENT      Location/Qualifiers
              source
                1..10
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CGGGCCCTAC 10
|||||
1 CGGGCCCTCC 10

RESULT 120
LOCUS      BD166783          10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166783
VERSION     BD166783.1 GI:27872595
KEYWORDS    JP 2002209591-A/328.
ORGANISM     Human liver disease-expressing genes
REFERENCE    1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE        Human liver disease-expressing genes
JOURNAL      Patent: JP 2002209591-A 328 30-JUL-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2002209591-A/328
              PD 30-JUL-2002
              PF 19-JAN-2001 JP 2001012328
              PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
              YAMASHITA
              PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
              PC C12P21/08,
              PC C12N15/00
              CC Human liver disease-expressing genes
              FH Key
              FT source
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Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CGGGCCCTCC 10
|||||
1 CGGGCCCTCC 1

RESULT 121
LOCUS      BD167020/c        10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167020
VERSION     BD167020.1 GI:27872832
KEYWORDS    JP 2002209591-A/565.
ORGANISM     Human liver disease-expressing genes
REFERENCE    1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE        Human liver disease-expressing genes
JOURNAL      Patent: JP 2002209591-A 565 30-JUL-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2002209591-A/565
              PD 30-JUL-2002
              PF 19-JAN-2001 JP 2001012328
              PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
              YAMASHITA
              PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
              PC C12P21/08,
              PC C12N15/00
              CC Human liver disease-expressing genes
              FH Key
              FT source
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                /organism="Homo sapiens (human)"

Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

17 AGGAGTCCA 26
|||||
10 AGGGGTCCA 1

RESULT 122
LOCUS      BD167059/c        10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167059
VERSION     BD167059.1 GI:27872871
KEYWORDS    JP 2002209591-A/604.
ORGANISM     Human liver disease-expressing genes
REFERENCE    1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE        Human liver disease-expressing genes
JOURNAL      Patent: JP 2002209591-A 604 30-JUL-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2002209591-A/604
              PD 30-JUL-2002
              PF 19-JAN-2001 JP 2001012328
              PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
              YAMASHITA
              PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
              PC C12P21/08,
              PC C12N15/00
              CC Human liver disease-expressing genes
              FH Key
              FT source
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                /organism="Homo sapiens (human)"

Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

17 AGGAGTCCA 26
|||||
10 AGGGGTCCA 1

RESULT 123
LOCUS      BD167059/c        10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167059
VERSION     BD167059.1 GI:27872871
KEYWORDS    JP 2002209591-A/604.
ORGANISM     Human liver disease-expressing genes
REFERENCE    1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE        Human liver disease-expressing genes
JOURNAL      Patent: JP 2002209591-A 604 30-JUL-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2002209591-A/604
              PD 30-JUL-2002
              PF 19-JAN-2001 JP 2001012328
              PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
              YAMASHITA
              PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
              PC C12P21/08,
              PC C12N15/00
              CC Human liver disease-expressing genes
              FH Key
              FT source
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                /organism="Homo sapiens (human)"

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Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

17 AGGAGTCCA 26
|||||
10 AGGGGTCCA 1

RESULT 121
LOCUS      BD167020/c        10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167020
VERSION     BD167020.1 GI:27872832
KEYWORDS    JP 2002209591-A/565.
ORGANISM     Human liver disease-expressing genes
REFERENCE    1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE        Human liver disease-expressing genes
JOURNAL      Patent: JP 2002209591-A 565 30-JUL-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2002209591-A/565
              PD 30-JUL-2002
              PF 19-JAN-2001 JP 2001012328
              PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
              YAMASHITA
              PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
              PC C12P21/08,
              PC C12N15/00
              CC Human liver disease-expressing genes
              FH Key
              FT source
                1..10
                /organism="Homo sapiens (human)"

Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

17 AGGAGTCCA 26
|||||
10 AGGGGTCCA 1

RESULT 122
LOCUS      BD167059/c        10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167059
VERSION     BD167059.1 GI:27872871
KEYWORDS    JP 2002209591-A/604.
ORGANISM     Human liver disease-expressing genes
REFERENCE    1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE        Human liver disease-expressing genes
JOURNAL      Patent: JP 2002209591-A 604 30-JUL-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2002209591-A/604
              PD 30-JUL-2002
              PF 19-JAN-2001 JP 2001012328
              PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
              YAMASHITA
              PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
              PC C12P21/08,
              PC C12N15/00
              CC Human liver disease-expressing genes
              FH Key
              FT source
                1..10
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Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

17 AGGAGTCCA 26
|||||
10 AGGGGTCCA 1

RESULT 123
LOCUS      BD167059/c        10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167059
VERSION     BD167059.1 GI:27872871
KEYWORDS    JP 2002209591-A/604.
ORGANISM     Human liver disease-expressing genes
REFERENCE    1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE        Human liver disease-expressing genes
JOURNAL      Patent: JP 2002209591-A 604 30-JUL-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2002209591-A/604
              PD 30-JUL-2002
              PF 19-JAN-2001 JP 2001012328
              PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
              YAMASHITA
              PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
              PC C12P21/08,
              PC C12N15/00
              CC Human liver disease-expressing genes
              FH Key
              FT source
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                /organism="Homo sapiens (human)"

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PC C12N15/00,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 18 GGGAGTCCAG 27
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Db 10 GGGAGGCCAG 1

RESULT 123
LOCUS BD167158 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167158
VERSION BD167158.1 GI:27872970
KEYWORDS JP 2002209591-A/703.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamaehita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 703 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/703
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
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   Location/Qualifiers
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   /organism='unidentified'
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   /db_xref='taxon:32644'

Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 18 GGGAGTCCAG 27
   |||||
Db 10 GGGAGGCCAG 1

RESULT 124
LOCUS AR099559 11 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 86 from patent US 6077833.
ACCESSION AR099559
VERSION AR099559.1 GI:12809325
KEYWORDS

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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Bennett,C.Frank. and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
expression of B7 protein
JOURNAL Patent: US 6077833-A 86 20-JUN-2000;
FEATURES Location/Qualifiers
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   /mol_type='unassigned DNA'

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 13 GTACAGGGAG 22
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Db 11 GTACGGGGAG 2

RESULT 125
LOCUS AR178840 11 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 86 from patent US 6319906.
ACCESSION AR178840
VERSION AR178840.1 GI:20219978
KEYWORDS SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Bennett,C.Frank. and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
expression of B7 protein
JOURNAL Patent: US 6319906-A 86 20-NOV-2001;
FEATURES Location/Qualifiers
   source 1..11
   /organism='unknown'
   /mol_type='unassigned DNA'

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 13 GTACAGGGAG 22
   |||||
Db 11 GTACGGGGAG 2

RESULT 126
LOCUS BD241058 11 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and products related to genotyping and DNA analysis.
ACCESSION BD241058
VERSION BD241058.1 GI:33050828
KEYWORDS JP 2002525127-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 11)
AUTHORS Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.
TITLE Methods and products related to genotyping and DNA analysis
JOURNAL Patent: JP 2002525127-A 5 13-AUG-2002;
MASSACHUSETTS INSTITUTE OF TECHNOLOGY
COMMENT OS Homo sapiens (human)
PN JP 2002525127-A/5
PD 13-AUG-2002
PF 24-SEP-1999 JP 2000572407
PR 25-SEP-1998 US 60/101757
PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC

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C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/58, G01N37/00, PC  
 G01N37/00,  
 PC C12N15/00  
 CC Methods and products related to genotyping and DNA analysis FH  
 key Location/Qualifiers  
 FT source 1..11  
 ATURES Location/Qualifiers  
 source 1..11  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

8 TACGTGTACA 17  
 1 TACGTGTACA 10

RESULT 127  
 LOCUS AR301464 11 bp DNA linear PAT 12-JUN-2003  
 DEFINITION Sequence 45 from patent US 6538173.  
 ACCESSION AR301464  
 VERSION AR301464.1 GI:31689266  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 11)  
 AUTHORS Heber-Katz, E.  
 TITLE Compositions and methods for wound healing  
 JOURNAL Patent: US 6538173-A 45 25-MAR-2003;  
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 source 1..11  
 /organism="unknown"  
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Query Match 30.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

12 TGTACGGGGA 21  
 10 TGTACGGGGA 1

RESULT 128  
 LOCUS AX099043 11 bp DNA linear PAT 02-APR-2001  
 DEFINITION Sequence 106 from Patent WO0120026.  
 ACCESSION AX099043  
 VERSION AX099043.1 GI:13538253  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS Wojnowski, L. and Huster, E.  
 TITLE Polymorphisms in the human hpxr gene and their use in diagnostic  
 JOURNAL Patent: WO 0120026-A 106 22-MAR-2001;  
 EpiDauros Biotechnologie AG (DE)

FEATURES Location/Qualifiers  
 source 1..11  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="artificial sequence"

Query Match 30.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 GGGAGTCCAG 27  
 2 GGGAGTCCAG 11

RESULT 129  
 LOCUS AX099044 11 bp DNA linear PAT 02-APR-2001  
 DEFINITION Sequence 107 from Patent WO0120026.  
 ACCESSION AX099044  
 VERSION AX099044.1 GI:13538254  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS Wojnowski, L. and Huster, E.  
 TITLE Polymorphisms in the human hpxr gene and their use in diagnostic  
 JOURNAL Patent: WO 0120026-A 107 22-MAR-2001;  
 EpiDauros Biotechnologie AG (DE)

FEATURES Location/Qualifiers  
 source 1..11  
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 /db\_xref="taxon:32630"  
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Query Match 30.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 GGGAGTCCAG 27  
 10 GGGAGTCCAG 1

RESULT 130  
 LOCUS AX470626 11 bp DNA linear PAT 09-AUG-2002  
 DEFINITION Sequence 203 from Patent WO02053773.  
 ACCESSION AX470626  
 VERSION AX470626.1 GI:22205751  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Hofmann, K., Conrad, M. and Petersohn, D.  
 TITLE Method for determining skin stress or skin ageing in vitro  
 JOURNAL Patent: WO 02053773-A 203 11-JUL-2002;  
 HENKEL KGAA (DE)

FEATURES Location/Qualifiers  
 source 1..11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

13 GTACAGGAG 22  
 10 GTTACAGGAG 1

RESULT 131

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AX470645
OCUS AX470645 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 222 from Patent WO02053773.
CESSION AX470645
ERSION AX470645.1 GI:22205770
EYWORDS Homo sapiens (human)
OURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 222 11-JUL-2002;
HENKEL KGAA (DE)
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1. .11
Location/Qualifiers
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Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 1 CCGGCCCTAC 10
| | | | |
b 1 CCGGCCCTAC 10
1
RESULT 132
AX470757
OCUS AX470757 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 334 from Patent WO02053773.
CESSION AX470757
ERSION AX470757.1 GI:22205882
EYWORDS Homo sapiens (human)
OURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 334 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 18 GGGAGTCCAG 27
| | | | |
b 2 GGGAGTCCAG 11
1
RESULT 133
AX470853
OCUS AX470853 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 430 from Patent WO02053773.
CESSION AX470853
ERSION AX470853.1 GI:22205978
EYWORDS Homo sapiens (human)
OURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE

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AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 430 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 19 GGAGTCCAGG 28
| | | | |
b 2 GGAGTCCAGG 11
1
RESULT 134
AX471193/c
LOCUS AX471193 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 770 from Patent WO02053773.
CESSION AX471193
ERSION AX471193.1 GI:22206318
EYWORDS Homo sapiens (human)
OURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 770 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
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Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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b 11 CAGTGAATCC 2
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RESULT 135
AX472098
LOCUS AX472098 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 89 from Patent WO02053775.
CESSION AX472098
ERSION AX472098.1 GI:22207139
EYWORDS Homo sapiens (human)
OURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Hustert,E., Haberl,M. and Wojnowski,L.
TITLE Identification of the genetic determinants of the polymorphic
JOURNAL cyp3a5 expression
Patent: WO 02053775-A 89 11-JUL-2002;
EPIDAURUS BIOTECHNOLOGIE AG (DE)
FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

13 GTACAGGAG 22
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1 GTACAGGAG 10

SULT 136
623332
CUS AX623332 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 373 from Patent WO02053774.
ACCESSION AX623332
VERSION AX623332.1 GI:28451273
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 373 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

4 GCCCTACGCTG 13
|||||
1 GCCCTACGCTG 10

SULT 137
623370/c
CUS AX623370 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 411 from Patent WO02053774.
ACCESSION AX623370
VERSION AX623370.1 GI:28451311
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 411 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 GGGAGTCCAG 27
|||||
11 GGGAGTCAAG 2

SULT 138
623664/c
CUS AX623664 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 705 from Patent WO02053774.
ACCESSION AX623664
VERSION AX623664.1 GI:28451605
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 705 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

11 GTGTACAGG 20
|||||
11 GAGTACAGG 2

RESULT 139
AX623917
LOCUS AX623917 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 958 from Patent WO02053774.
ACCESSION AX623917
VERSION AX623917.1 GI:28451858
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 958 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

19 GGAGTCCAGG 28
|||||
2 GGATCCAGG 11

RESULT 140
AX624031/c
LOCUS AX624031 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1072 from Patent WO02053774.
ACCESSION AX624031
VERSION AX624031.1 GI:28451972
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS

```



TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 1072 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 13 GTACAGGAG 22  
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Db 10 GTTACGGAG 1

RESULT 141  
LOCUS AX624952 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 1993 from Patent WO02053774.  
ACCESSION AX624952  
VERSION AX624952.1 GI:28452893  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 1993 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CGGGCCCTAC 10  
| | | | |  
Db 1 CGGGCCCTAC 10

RESULT 142  
LOCUS AX625222/c 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 2263 from Patent WO02053774.  
ACCESSION AX625222  
VERSION AX625222.1 GI:28453163  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 2263 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.1e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 9 ACGGTACAG 18  
| | | | |  
Db 11 AGGTGTACAG 2

RESULT 143  
LOCUS AX625736 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 2777 from Patent WO02053774.  
ACCESSION AX625736  
VERSION AX625736.1 GI:28453677  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 2777 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27  
| | | | |  
Db 2 GGGACTCCAG 11

RESULT 144  
LOCUS AX627101 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 4142 from Patent WO02053774.  
ACCESSION AX627101  
VERSION AX627101.1 GI:28455139  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 4142 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGG 20  
| | | | |  
Db 2 GTGTTCAGG 11

RESULT 145  
LOCUS AX629184 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 6225 from Patent WO02053774.

Henkel Kommanditgesellschaft auf Aktien (DE)					
FEATURES					
source					
1. .11 Location/Qualifiers /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"					
Query Match 30.0%; Score 8.4; DB 1; Length 11;					
Best Local Similarity 90.0%; Pred. No. 1.1e+02;					
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY 16 CAGGGAGTCC 25					
DB 11 CASTGAGTCC 2					
RESULT 148					
AXG30753					
LOCUS					
Sequence 7794 from Patent WO02053774.					
DEFINITION AXG30753					
ACCESSION					
VERSION AXG30753.1 GI:28458791					
KEYWORDS					
SOURCE Homo sapiens (human)					
ORGANISM					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini, Hominiidae; Homo. 1 Petersohn,D., Conradt,M. and Hofmann,K. Method for determining homeostasis of the skin Patent: WO 02053774-A 7794 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers 1. .11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"					
FEATURES					
source					
1. .11 Location/Qualifiers /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"					
Query Match 30.0%; Score 8.4; DB 1; Length 11;					
Best Local Similarity 90.0%; Pred. No. 1.1e+02;					
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY 4 GCCCTACTGT 13					
DB 1 GCCCTACTGT 10					
RESULT 149					
AXG30791/C					
LOCUS					
Sequence 7832 from Patent WO02053774.					
DEFINITION AXG30791					
ACCESSION					
VERSION AXG30791.1 GI:28458831					
KEYWORDS					
SOURCE Homo sapiens (human)					
ORGANISM					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini, Hominiidae; Homo. 1 Petersohn,D., Conradt,M. and Hofmann,K. Method for determining homeostasis of the skin Patent: WO 02053774-A 7832 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers 1. .11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"					
FEATURES					
source					
1. .11 Location/Qualifiers /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"					
Query Match 30.0%; Score 8.4; DB 1; Length 11;					
Best Local Similarity 90.0%; Pred. No. 1.1e+02;					
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					

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Y 18 GGGAGTCCAG 27
b 11 GGGAGTCCAG 2

RESULT 150
X631085/c
OCUS
DEFINITION
TITLE
JOURNAL
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 8126 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 11 GTGTACAGGG 20
b 11 GAGTACAGGG 2

RESULT 151
X631338
OCUS
DEFINITION
TITLE
JOURNAL
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 8380 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 11 GTGTACAGGG 20
b 11 GAGTACAGGG 2

RESULT 152
X631452/c
OCUS
DEFINITION
TITLE
JOURNAL
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 8494 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 19 GGAGTCCAGG 28
b 2 GGAATCCAGG 11

RESULT 153
X632373
OCUS
DEFINITION
TITLE
JOURNAL
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 9415 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 13 GTACAGGGAG 22
b 10 GTTCAGGGAG 1

RESULT 154
X632643/c
OCUS
DEFINITION
TITLE
JOURNAL
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 9685 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
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Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CGGGCCCTAC 10
b 1 CCGGCCCTAC 10

RESULT 155
X6332643
OCUS
DEFINITION
TITLE
JOURNAL
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 9685 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CGGGCCCTAC 10
b 1 CCGGCCCTAC 10

RESULT 156
X6332643
OCUS
DEFINITION
TITLE
JOURNAL
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 9685 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CGGGCCCTAC 10
b 1 CCGGCCCTAC 10

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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8494 11-JUL-2002; (DE)
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 13 GTACAGGGAG 22
b 10 GTTCAGGGAG 1

RESULT 153
X632373
LOCUS
DEFINITION
Sequence 9415 from Patent WO02053774.
ACCESSION
X632373
VERSION
X632373.1 GI:28467988
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9415 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CGGGCCCTAC 10
b 1 CCGGCCCTAC 10

RESULT 154
X632643/c
LOCUS
DEFINITION
Sequence 9685 from Patent WO02053774.
ACCESSION
X632643
VERSION
X632643.1 GI:28469258
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9685 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
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Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 11;
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Y 1 CGGGCCCTAC 10
b 1 CCGGCCCTAC 10

RESULT 155
X6332643/c
LOCUS
DEFINITION
Sequence 9685 from Patent WO02053774.
ACCESSION
X6332643
VERSION
X6332643.1 GI:28469258
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9685 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
source /organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CGGGCCCTAC 10
b 1 CCGGCCCTAC 10

RESULT 156
X6332643
OCUS
DEFINITION
Sequence 9685 from Patent WO02053774.
ACCESSION
X6332643
VERSION
X6332643.1 GI:28469258
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9685 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CGGGCCCTAC 10
b 1 CCGGCCCTAC 10

RESULT 157
X6332643
OCUS
DEFINITION
Sequence 9685 from Patent WO02053774.
ACCESSION
X6332643
VERSION
X6332643.1 GI:28469258
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9685 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CGGGCCCTAC 10
b 1 CCGGCCCTAC 10

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## source

1. .11  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 30.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 9 ACCTGATACAG 18  
 |||||  
 11 AGCTGTACAG 2

## SULT 155

124214/c  
 CUS 11 bp DNA linear PAT 18-SEP-2002  
 FINITION Compositions and method for healing wound.  
 CESSION BD124214  
 RSION BD124214.1 GI:23219159  
 YWORDS JP 2002503460-A/45.  
 ORGANCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Katz, B.H.  
 1 (bases 1 to 11)  
 Compositions and method for healing wound  
 Patent: JP 2002503460-A 45 05-FEB-2002;  
 THE WISTAR INSTITUTE  
 OS Mus musculus (mouse)  
 PN JP 2002503460-A/45  
 PD 05-FEB-2002  
 PR 12-FEB-1999 JP 2000531545  
 PR 13-FEB-1998 US 60/074737, 26-AUG-1998 US 60/097937 PR  
 28-SEP-1998 US 60/102051  
 PI ELLEN HEEB KATZ  
 PC C12N15/09, A01K67/027, C12N5/10, C12Q1/68, G01N33/50, C12N15/00, PC  
 C12N5/00

## MMENT

CC Compositions and method for healing wound  
 FH Key Location/Qualifiers  
 FT source 1. .11  
 /organism="Mus musculus (mouse)"  
 FT Location/Qualifiers  
 1. .11  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"

## FEATURES

## source

Query Match 30.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 12 TGTACGGGGA 21  
 |||||  
 10 TGTACGGGGA 1

## RESULT 156

17668/c  
 JCUS 12 bp DNA linear PAT 07-MAR-1997  
 FINITION Sequence 28 from Patent EP0692535.  
 CESSION A47668  
 RSION A47668.1 GI:2301609  
 YWORDS  
 SOURCE unidentified  
 ORGANISM unidentified  
 1 (bases 1 to 12)  
 Colote, S. and Pirotzky, E.  
 Oligonucleotides to inhibit the role of isoprenyl protein  
 transferases  
 Patent: EP 0692535-A 28 17-JAN-1996;

## COMMENT

SOD CONSEILS RECH APPLIC (FR)  
 Other publication CN 1124142 960612  
 Other publication CZ 9501688 960515  
 Other publication BR 9503015 960604  
 Other publication NZ 272398 960426  
 Other publication HU 72133 960328  
 Other publication JP 851985 960227  
 Other publication FR 2721930 960105  
 Other publication FR 2721827 960105  
 Other publication FI 953170 951230  
 Other publication SE 9502259 951230  
 Other publication PL 309384 960108  
 Other publication NO 952601 960102  
 Other publication AU 232995 960111  
 Other publication CA 215223 951230  
 Other publication GB 2290791 960110.

## FEATURES

## source

1. .12  
 /organism="unidentified"  
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Query Match 30.0%; Score 8.4; DB 1; Length 12;  
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 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## Qy 9 ACCTGTACAG 18

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## Db 11 ACAGTACAG 2

## RESULT 157

AR024089  
 LOCUS AR024089 12 bp DNA linear PAT 05-DEC-1998  
 DEFINITION Sequence 39 from patent US 5795778.  
 ACCESSION AR024089  
 VERSION AR024089.1 GI:39777383  
 KEYWORDS  
 SOURCE Unknown.

## ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 12)

AUTHORS Draper, K.G.

TITLE Method and reagent for inhibiting herpes simplex virus replication

JOURNAL Patent: US 5795778-A 39 18-AUG-1998;

## FEATURES

## source

1. .12  
 Location/Qualifiers  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

## Query Match

30.0%; Score 8.4; DB 1; Length 12;

## Best Local Similarity

90.0%; Pred. No. 1.3e+02;

## Matches

9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## Qy 5 CCTTACGTGT 14

|||||

## Db 1 CCCGACGTGT 10

## RESULT 158

AR027886/c  
 LOCUS AR027886 12 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 28 from patent US 5856461.  
 ACCESSION AR027886  
 VERSION AR027886.1 GI:5938706  
 KEYWORDS  
 SOURCE Unknown.

## ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 12)

AUTHORS Colote, S. and Pirotzky, E.

TITLE Oligonucleotides to inhibit the expression of isoprenyl protein

transferases

RESULT 161	ARL78738	12 bp	DNA	linear	PAT 20-APR-2002
LOCUS	Sequence 25 from patent US 6319714.				
DEFINITION	ARL78738				
ACCESSION	ARL78738				
VERSION	GI:20219876				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 12)				
AUTHORS	Cramer, A., Stemmer, W.P.C., Minshull, J., Bass, S.H., Welch, M.,				
TITLE	Ness, J.E., Gustafsson, C. and Patten, P.A.				
JOURNAL	Oligonucleotide mediated nucleic acid recombination				
FEATURES	Patent: US 6319714-A 25 20-NOV-2001;				
source	Location/Qualifiers				
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	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	30.0%; Score 8.4; DB 1; Length 12;				
Best Local Similarity	90.0%; Pred. No. 1.3e+02;				
Matches	9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	18 GGGAGTCCAG 27				
Db	2 GGGGTCCAG 11				
RESULT 162	ARL78841	12 bp	DNA	linear	PAT 20-APR-2002
LOCUS	Sequence 87 from patent US 6319906.				
DEFINITION	ARL78841				
ACCESSION	ARL78841				
VERSION	GI:20219979				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 12)				
AUTHORS	Bennett, C. Frank and Vickers, T.A.				
TITLE	Oligonucleotide compositions and methods for the modulation of the				
JOURNAL	expression of B7 protein				
FEATURES	Patent: US 6319906-A 87 20-NOV-2001;				
source	Location/Qualifiers				
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	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	30.0%; Score 8.4; DB 1; Length 12;				
Best Local Similarity	90.0%; Pred. No. 1.3e+02;				
Matches	9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	13 GTACAGGGAG 22				
Db	12 GTACGGGGAG 3				
RESULT 163	BD251252	12 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	Oligonucleotide mediated nucleic acid recombination.				
DEFINITION	BD251252				
ACCESSION	BD251252				
VERSION	GI:33061022				
KEYWORDS	JP 2002534966-A/25.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
	1 (bases 1 to 12)				
	Cramer, A., Stemmer, W.P.C., Minshull, J., Bass, S.H., Welch, M.,				
	Ness, J.E., Gustafsson, C. and Patten, P.A.				

TITLE Oligonucleotide mediated nucleic acid recombination  
JOURNAL  
PATENT: JP 2002534966-A 25 22-OCT-2002;

MMENT OS Homo sapiens (human)

PN JP 2002534966-A/25

PD 22-OCT-2002

PF 18-JAN-2000 JP 2000594068

PR 19-JAN-1999 US 60/116447, 05-FEB-1999 US 60/118813 PR

OS-FEB-1999 US 60/118854, 24-JUN-1999 US 60/141049 PR

28-SEP-1999 US 09/408392, 28-SEP-1999 US 09/408393 PR

12-OCT-1999 US 09/416375, 12-OCT-1999 US 09/416837 FI

ANDREAS CRAMER, WILLEM P C STENNER, JEREMY MINSHULL, STEVEN H PI

PI MARK WELCH, JON E NESS, CLAES GUSTAFSSON, PHILLIP A PATTEN PC

C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N7/00, C12Q1/ PC

68, C12N15/00

PC C12N5/00

CC Oligonucleotide mediated nucleic acid recombination PH Key

FT CDS Location/Qualifiers

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Location/Qualifiers

1..12

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 1.3e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 GGGAGTCCAG 27

2 GGGGTCCAG 11

RESULT 164

9627/c

LOCUS 12 bp DNA linear PAT 18-JUN-2001

DEFINITION Method for amplifying DNA fragment, method for estimating state of

microorganism existing and method for estimating state of waste.

E29627

E29627.1 GI:13021130

JP 1999276175-A/107.

unidentified

unclassified

1 (bases 1 to 12)

Koichi, I.

Method for amplifying DNA fragment, method for estimating state of

microorganism existing and method for estimating state of waste

PATENT: JP 1999276175-A 107 12-OCT-1999;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE

FORESTRY AND FISHERIES

OS Unidentified

PN JP 1999276175-A/107

PD 12-OCT-1999

PF 31-MAR-1998 JP 1999087652

PR KOICHI INOUE

PC C12N15/09, B09B3/00, C12Q1/00, C12Q1/68, C12N15/00, B09B3/00 CC

Strandedness: Single; Location/Qualifiers

PH Key

FT source

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Location/Qualifiers

/organism="Unidentified"

1..12

/organism="unidentified"

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/db\_xref="taxon:32644"

Query Match 30.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 1.3e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 GGGAGTCCAG 27

2 GGGGTCCAG 11

RESULT 164

9627/c

LOCUS 12 bp DNA linear PAT 18-JUN-2001

DEFINITION Method for amplifying DNA fragment, method for estimating state of

microorganism existing and method for estimating state of waste

PATENT: JP 1999276175-A 107 12-OCT-1999;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE

FORESTRY AND FISHERIES

OS Unidentified

PN JP 1999276175-A/107

PD 12-OCT-1999

PF 31-MAR-1998 JP 1999087652

PR KOICHI INOUE

PC C12N15/09, B09B3/00, C12Q1/00, C12Q1/68, C12N15/00, B09B3/00 CC

Strandedness: Single; Location/Qualifiers

QY 7 CTACGTGTAC 16

Db 12 CTTCGTGTAC 3

RESULT 165

E38733/c

LOCUS 12 bp DNA linear PAT 31-JAN-2002

DEFINITION Method and device for amplifying DNA fragment.

E38733

E38733.1 GI:18621395

JP 2000270867-A/107.

unidentified

unclassified

1 (bases 1 to 12)

Inoue, K

Method and device for amplifying DNA fragment

PATENT: JP 2000270867-A 107 03-OCT-2000;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE

FORESTRY AND FISHERIES

OS Unidentified

PN JP 2000270867-A/107

PD 03-OCT-2000

PF 19-MAR-1999 JP 1999076844

PR KOICHI INOUE

PC C12N15/09, C12M1/00, C12Q1/68, C12N15/00

Strandedness: Single;

CC Topology: Linear;

PH Key

FT source

1..12

Location/Qualifiers

/organism="Unidentified"

1..12

Location/Qualifiers

/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

Query Match 30.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 1.3e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

7 CTACGTGTAC 16

12 CTTCGTGTAC 3

RESULT 166

E64159/c

LOCUS 12 bp DNA linear PAT 18-JUN-2001

DEFINITION Method for amplifying DNA fragment, amplification apparatus of DNA

fragment, method for assaying a group of microorganisms, method

for analyzing a group of microorganisms, and method for assaying

contaminating substance.

E64159

E64159.1 GI:13019563

JP 1999341989-A/107.

synthetic construct

synthetic construct

artificial sequences.

1 (bases 1 to 12)

Koichi, I.

Method for amplifying DNA fragment, amplification apparatus of DNA

fragment, method for assaying a group of microorganisms, method for

analyzing a group of microorganisms, and method for assaying

contaminating substance

PATENT: JP 1999341989-A 107 14-DEC-1999;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE

FORESTRY AND FISHERIES

OS Artificial Sequence

PN JP 1999341989-A/107

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PD 14-DEC-1999
PF 16-MAR-1999 JP 1999069694
PR KOICHI INOUE
PI C12N15/09,C12M1/00,C12Q1/68,C12N15/00
PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
CC Key Location/Qualifiers
EH source 1..12
FT Location/Qualifiers
FT source 1..12
  /organism='Artificial Sequence'
  /organism='synthetic construct'
  /mol_type='genomic DNA'
  /db_xref='taxon:32630'

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 7 CTACGGTGATC 16
  ||| |||||
  12 CTTCGGTGATC 3

RESULT 167
R205443
LOCUS AR205443 12 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 25 from patent US 636861.
ACCESSION AR205443
VERSION AR205443.1 GI:21503026
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Cramer,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
Ness,J.E., Gustafsson,C. and Patten,P.A.
TITLE Oligonucleotide mediated nucleic acid recombination
JOURNAL Patent: US 636861-A 25 09-APR-2002;
FEATURES
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Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 18 GGGAGTCCAG 27
  ||| |||||
  2 GGGGGTCCAG 11

RESULT 168
R220135
LOCUS AR220135 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 25 from patent US 6423542.
ACCESSION AR220135
VERSION AR220135.1 GI:23324577
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Cramer,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
Ness,J.E., Gustafsson,C. and Patten,P.A.
TITLE Oligonucleotide mediated nucleic acid recombination
JOURNAL Patent: US 6423542-A 25 23-JUL-2002;
FEATURES
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    Location/Qualifiers
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        /organism='unknown'
        /mol_type='genomic DNA'

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Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27
  ||| |||||
  2 GGGGGTCCAG 11

RESULT 169
R221524
LOCUS AR221524 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 25 from patent US 6426224.
ACCESSION AR221524
VERSION AR221524.1 GI:23328574
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Cramer,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
Ness,J.E., Gustafsson,C. and Patten,P.A.
TITLE Oligonucleotide mediated nucleic acid recombination
JOURNAL Patent: US 6426224-A 25 30-JUL-2002;
FEATURES
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    Location/Qualifiers
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        /organism='unknown'
        /mol_type='genomic DNA'

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27
  ||| |||||
  2 GGGGGTCCAG 11

RESULT 170
R224308
LOCUS AR224308 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 39 from patent US 6440719.
ACCESSION AR224308
VERSION AR224308.1 GI:23333085
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting herpes simplex virus replication
JOURNAL Patent: US 6440719-A 39 27-AUG-2002;
FEATURES
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    Location/Qualifiers
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        /organism='unknown'
        /mol_type='genomic DNA'

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCTACGTGT 14
  ||| |||||
  1 CCCGACGTGT 10

RESULT 171
R254226
LOCUS AR254226 12 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 25 from patent US 6479652.
ACCESSION AR254226
VERSION AR254226.1 GI:27302963
KEYWORDS

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URCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Cramer, A., Stemmer, W.P.C., Minshull, J., Bass, S.H., Welch, M.,
Ness, J.E., Gustafsson, C. and Patten, P.A.
TITLE Oligonucleotide mediated nucleic acid recombination
JOURNAL Patent: US 6479652-A 25 12-NOV-2002;
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            /mol_type="genomic DNA"

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 GGGAGTCCAG 27
|||||
2 GGGGTCAG 11

SULT 172
282432
CUS AR282432 12 bp DNA linear PAT 10-APR-2003
FINITION Sequence 25 from patent US 6521453.
CESSION AR282432
RSION AR282432.1 GI:29718598
WORDS
URCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Cramer, A., Stemmer, W.P.C., Minshull, J., Bass, S.H., Welch, M.,
Ness, J.E., Gustafsson, C. and Patten, P.A.
TITLE Oligonucleotide mediated nucleic acid recombination
JOURNAL Patent: US 6521453-A 25 18-FEB-2003;
FEATURES
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            /mol_type="genomic DNA"

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 GGGAGTCCAG 27
|||||
2 GGGGTCAG 11

SULT 173
1368339
CUS AR368339 12 bp DNA linear PAT 12-SEP-2003
FINITION Sequence 25 from patent US 6376246.
CESSION AR368339
RSION AR368339.1 GI:34602023
WORDS
URCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Cramer, A., Stemmer, W.P.C., Minshull, J., Bass, S.H., Welch, M.,
Ness, J.E., Gustafsson, C. and Patten, P.A.
TITLE Oligonucleotide mediated nucleic acid recombination
JOURNAL Patent: US 6376246-A 25 23-APR-2002;
FEATURES
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            /mol_type="genomic DNA"

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27
|||||
DB 2 GGGGTCAG 11

RESULT 174
AX463121/c
LOCUS AX463121 12 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 4 from Patent WO0250108.
ACCESSION AX463121
VERSION AX463121.1 GI:21886102
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Marchal, G., Pescher, P. and Romain, F.
TITLE Immunogenic glycopeptides, screening, preparation and uses
JOURNAL Patent: WO 0250108-A 4 27-JUN-2002;
PASTEUR INSTITUT (FR)
FEATURES
    source
        1..12
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGCCTACGT 12
|||||
DB 12 GGCCCAAGT 3

RESULT 175
AX711090
LOCUS AX711090 12 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 390 from Patent EP1288296.
ACCESSION AX711090
VERSION AX711090.1 GI:29787471
KEYWORDS Herpes simplex virus unknown type
SOURCE Herpes simplex virus unknown type
ORGANISM Herpes simplex virus unknown type
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
REFERENCE 1
AUTHORS Draper, K.G., McSwiggen, J.A., Holecek, J.J., Dudycz, L.W.,
Macejak, D.G. and Mamone, J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 390 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
    source
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            /mol_type="unassigned RNA"
            /db_xref="taxon:126283"

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCCTACGTGT 14
|||||
DB 1 CCCGACGTGT 10

RESULT 176
BD001193
LOCUS BD001193 12 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.

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CESSION BD001193
ERSON BD001193.1 GI:18625752
YWORDS JP 2000342285-A/353.
OURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Draper,K.G., Dadykztz,L.W., Macswigen,J.A., Maysejak,D.G.,
Holesek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342285-A 353 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
OMMENT OS Artificial Sequence
PN JP 2000342285-A/353
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132616
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
15-OCT-1992 US 07/987130,07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER,LEC W DADYKZT,JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK,ANTHONY J MAMONE
PC C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
PC A61K39/135,
PC A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
PC A61P1/16
PC A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12O1/69,PC
(C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00,PC
C12R1:93)
CC
PH Key Location/Qualifiers
FT source 1..12
FEATURES
source
Location/Qualifiers
1..12
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 CCTACGTGT 14
Db 1 CCCGACGTGT 10
RESULT 178
AR165205/c
LOCUS AR165205 21 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 19 from patent US 6274708.
ACCESSION AR165205
VERSION AR165205.1 GI:16238680
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hilton,D.James.
TITLE Mouse interleukin-11 receptor
JOURNAL Patent: US 6274708-A 19 14-AUG-2001;
FEATURES
source
Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 29.3%; Score 8.2; DB 1; Length 21;
Best Local Similarity 76.9%; Pred. No. 2.8e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 7 CTACGTGTACAG 19
Db 15 CTCCAAGTACAG 3

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SULT 179
456625/c
CUS AX456625 9 bp DNA linear PAT 06-JUL-2002
FINITION Sequence 97 from Patent WO0218407.
CESSION AX456625
RSION AX456625.1 GI:21715512
WORDS
URCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1
REFERENCE Kurreck, J. and Erdmann, V.A.
AUTHORS
TITLE Antisense oligonucleotides against vrl
JOURNAL Patent: WO 0218407-A 97 07-MAR-2002;
Gruenthal GmbH (DE)
ATUES Location/Qualifiers
source
1. .9
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"

Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 GGAGTCCA 26
|||||
9 GGAGTCCA 2

SULT 180
668649/c
CUS AX668649 9 bp DNA linear PAT 26-MAR-2003
FINITION Sequence 2098 from Patent WO0242459.
CESSION AX668649
RSION AX668649.1 GI:29291624
WORDS
URCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE Liu, Q.
AUTHORS
TITLE Position dependent recognition of gnm nucleotide triplets by zinc
JOURNAL Patent: WO 0242459-A 2195 30-MAY-2002;
Sangamo Biosciences Inc. (US)
ATUES Location/Qualifiers
source
1. .9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="example target DNA"

Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 CCCTACGT 12
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9 CCCTACGT 2

SULT 181
668651/c
CUS AX668651 9 bp DNA linear PAT 26-MAR-2003
FINITION Sequence 2100 from Patent WO0242459.
CESSION AX668651
RSION AX668651.1 GI:29291626
WORDS
URCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE Liu, Q.
AUTHORS
TITLE Position dependent recognition of gnm nucleotide triplets by zinc
JOURNAL Patent: WO 0242459-A 2453 30-MAY-2002;
Sangamo Biosciences Inc. (US)
ATUES Location/Qualifiers
source
1. .9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="example target DNA"

Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 CCCTACGT 12
|||||
9 CCCTACGT 2

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artificial sequences.
1
REFERENCE Liu, Q.
AUTHORS
TITLE Position dependent recognition of gnm nucleotide triplets by zinc
JOURNAL Patent: WO 0242459-A 2100 30-MAY-2002;
Sangamo Biosciences Inc. (US)
ATUES Location/Qualifiers
source
1. .9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="example target DNA"

Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 CCCTACGT 12
|||||
9 CCCTACGT 2

RESULT 182
AX668746
LOCUS AX668746 9 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2195 from Patent WO0242459.
ACCESSION AX668746
VERSION AX668746.1 GI:29291721
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE Liu, Q.
AUTHORS
TITLE Position dependent recognition of gnm nucleotide triplets by zinc
JOURNAL Patent: WO 0242459-A 2195 30-MAY-2002;
Sangamo Biosciences Inc. (US)
ATUES Location/Qualifiers
source
1. .9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="example target DNA"

Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

17 AGGAGTC 24
|||||
2 AGGAGTC 9

RESULT 183
AX669004/c
LOCUS AX669004 9 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2453 from Patent WO0242459.
ACCESSION AX669004
VERSION AX669004.1 GI:29291981
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE Liu, Q.
AUTHORS
TITLE Position dependent recognition of gnm nucleotide triplets by zinc
JOURNAL Patent: WO 0242459-A 2453 30-MAY-2002;
Sangamo Biosciences Inc. (US)
ATUES Location/Qualifiers
source
1. .9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="example target DNA"

Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

17 AGGAGTC 24
|||||
2 AGGAGTC 9

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="example target DNA"

Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CGGGCCCT 8
b 9 CGGGCCCT 2

RESULT 184
LOCUS AX669005 9 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2454 from Patent WO0242459.
ACCESSION AX669005
VERSION AX669005.1 GI:29291982
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1.
AUTHORS Liu,Q.
TITLE Position dependent recognition of gmn nucleotide triplets by zinc
JOURNAL
JOURNAL
FEATURES
source
1..9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="example target DNA"

Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CGGGCCCT 8
b 9 CGGGCCCT 2

RESULT 185
LOCUS A78814 10 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 12 from Patent EP0561245.
ACCESSION A78814
VERSION A78814.1 GI:6090408
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS Hoffman,S.J. and Nagai,K.
TITLE BLOOD SUBSTITUTES COMPRISING RECOMBINANT HEMOGLOBIN
JOURNAL
JOURNAL
FEATURES
Location/Qualifiers
1..10
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 CGGGCCCT 8
b 9 CGGGCCCT 2

RESULT 186
LOCUS BD238631 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238631
VERSION BD238631.1 GI:33049401
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL
JOURNAL
COMMENT
Patent: JP 2002534056-A 49 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/49
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N5/03,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 6 CCTACGTG 13
b 2 CCTACGTG 9

RESULT 187
LOCUS BD240218 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240218
VERSION BD240218.1 GI:33049988
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

PR	27-JAN-1999	EP	99400189.9
PI	LYDSE CHEVAL JEAN MARC ELALOUF BERANGERE VIELON	PC	C12N15/09,C12Q1/68,C12N15/00
CC	Microassay for continuous analysis of gene expression and its application		
CC	Key	Location/Qualifiers	
FT	source	1..10	/organism='Mus sp. (mouse)'
PT		Location/Qualifiers	
		1..10	/organism="Mus sp."
			/mol_type="genomic DNA"
			/db_xref="taxon:10095"
Query Match	28.6%; Score 8; DB 1; Length 10;		
Best Local Similarity	100.0%; Pred.No. 1.1e+02;		
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
17 AGCGGAGTC 24			
9 AGGGAGT 2			
E54660	Human normal liver cell expression genes.	10 bp	DNA linear PAT 27-AUG-2002
E54660			
E54660.1	GI:22556143		
JP 2001211883-A/12.			
Homo sapiens (human)			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 10)			
Katsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.			
Human normal liver cell expression genes			
Patent: JP 2001211883-A 12 07-AUG-2001;			
SCIENCE & TECH AGENCY			
OS Homo sapiens (human)			
PN JP 2001211883-A/12			
PD 07-AUG-2001			
PF 31-JAN-2000 JP 2000023170			
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI YAMASHITA			
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00			
CC			
FH Key	Location/Qualifiers.		
	Location/Qualifiers		
	1..10		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
Query Match	28.6%; Score 8; DB 1; Length 10;		
Best Local Similarity	100.0%; Pred.No. 1.1e+02;		
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
1 CGGGCCCT 8			
3 CGGGCCCT 10			
I63091	Sequence 12 from patent US 5661124.	10 bp	DNA linear PAT 07-OCT-1997
I63091			
I63091.1	GI:2480799		
Unknown.			
Unknown.			
Unclassified.			

Query Match	28.6%	Score 8;	DB 1;	Length 10;
Best Local Similarity	100.0%	Pred. No. 1.1e+02;		
Matches 8;	Conservative 0;	Mismatches 0;	Indels	

Accession	AX152759	linear	PAT 22-JUN-2001
Definition	Sequence 674 from Patent WO0138577.		
LOCUS	AX152759	10 bp	DNA
Accession	AX152759		

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FEATURES             Location/Qualifiers
   source              1..10
                        /organism="Homo sapiens"
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Query Match          28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.le+02;
Matches              8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 ACGGTGAC 16
        |||||
DB       10 ACGGTGAC 3

RESULT 198
AXX374632
LOCUS     AXX374632                10 bp    DNA            linear    PAT 01-MAR-2002
DEFINITION Sequence 53 from Patent WO0210454.
ACCESSION AXX374632
VERSION   AXX374632.1 GI:19169529
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Choi,J.Y., Koshy,B., Klien,S. and Stephens,J.C.
TITLE     Haplotypes of the alas2 gene
JOURNAL   Patent: WO 0210454-A 53 07-FEB-2002;
          Genaisance Pharmaceuticals, Inc. (US)

FEATURES             Location/Qualifiers
   source              1..10
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match          28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.le+02;
Matches              8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 AGTCCAGG 28
        |||||
DB       2 AGTCCAGG 9

RESULT 199
BD007893
LOCUS     BD007893                10 bp    DNA            linear    PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION  BD007893
VERSION     BD007893.1 GI:18636266
KEYWORDS    JP 2001069993-A/169,
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS     Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE       LPS activated human monocyte expressing genes
JOURNAL     Patent: JP 2001069993-A 169 21-MAR-2001;
           JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
           PN JP 2001069993-A/169
           PD 21-MAR-2001
           PF 28-APR-2000 JP 2000131079
PR          PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
           Cl2N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
           A6129/00
PC          A61P31/00,C12P21/08,C12N15/00
CC          CC
PH          PH Key Location/Qualifiers

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FEATURES
  source
    FT source 1..10 /organism='Homo sapiens (human)'.
    TITLE Location/Qualifiers
    JOURNAL 1..10
    COMMENT /organism='Homo sapiens'
      /mol_type='genomic DNA'
      /db_xref='taxon:9606'

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 6 CCTACGTG 13
  |||||
b 2 CCTACGTG 9

RESULT 200
D007921/c
OCUS
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007921
VERSION BD007921.1 GI:18636294
KEYWORDS JP 2001069993-A/197.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Matsushima.K., Hashimoto.S. and Suzuki.T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 197 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001069993-A/197
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI
PC C12N15/09, C07K14/47, C07K16/18, G01N33/53//A61K45/00, PC
A61P29/00,
CC A61P31/00, C12P21/08, C12N15/00
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
  source
    FT source 1..10 /organism='Homo sapiens'
    TITLE Location/Qualifiers
    JOURNAL 1..10
    COMMENT /organism='Homo sapiens'
      /mol_type='genomic DNA'
      /db_xref='taxon:9606'

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 9 ACGGTGATC 16
  |||||
b 10 ACGGTGATC 3

RESULT 201
D065273
OCUS
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065273
VERSION BD065273.1 GI:22610876
KEYWORDS JP 2001509017-A/209.
SOURCE Saccharomyces cerevisiae (baker's yeast)
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 10)

```

```

AUTHORS Veiculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Characterization of the yeast transcriptome
JOURNAL Patent: JP 2001509017-A 209 10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/209
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELICULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Saccharomyces cerevisiae (yeast)'.

FEATURES
  source
    FT source 1..10 /organism='Saccharomyces cerevisiae'
    TITLE Location/Qualifiers
    JOURNAL 1..10
    COMMENT /mol_type='genomic DNA'
      /db_xref='taxon:4932'

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 13 GTACAGGG 20
  |||||
b 1 GTACAGGG 8

RESULT 202
D083323/c
OCUS
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083323
VERSION BD083323.1 GI:22628933
KEYWORDS JP 2001327293-A/244.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Matsushima.K., Hashimoto.S., Suzuki.T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 244 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/244
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI
NAGAI
PC C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
CC CC
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens'
  /mol_type='genomic DNA'
  /db_xref='taxon:9606'

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 11 GTGTACAG 18
  |||||
b 9 GTGTACAG 2

RESULT 203
BD167068
LOCUS BD167068 10 bp DNA linear PAT 17-JAN-2003

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OCUS AX421267 11 bp DNA linear PAT 18-JUN-2002  
DEFINITION Sequence 15 from Patent WO0218641.  
ACCESSION AX421267  
VERSION AX421267.1 GI:21524675  
KEYWORDS synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Olaiasson,E.  
TITLE Detection of cyp3a4 and cyp2c9 polymorphisms  
JOURNAL Patent: WO 0218641-A 15 07-MAR-2002;  
Gemini Genomics PLC (GB)  
FEATURES Location/Qualifiers  
source 1..11  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide of the novel polymorphic site 461  
on the coding strand"  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
y 11 GTGTACAG 18  
|||||  
b 3 GTGTACAG 10  
RESULT 208  
AX421268/c  
OCUS AX421268 11 bp DNA linear PAT 18-JUN-2002  
DEFINITION Sequence 16 from Patent WO0218641.  
ACCESSION AX421268  
VERSION AX421268.1 GI:21524676  
KEYWORDS synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Olaiasson,E.  
TITLE Detection of cyp3a4 and cyp2c9 polymorphisms  
JOURNAL Patent: WO 0218641-A 16 07-MAR-2002;  
Gemini Genomics PLC (GB)  
FEATURES Location/Qualifiers  
source 1..11  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide of the novel polymorphic site 461  
on the non-coding strand"  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
y 11 GTGTACAG 18  
|||||  
b 9 GTGTACAG 2  
RESULT 209  
AX470469/c  
OCUS AX470469 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 46 from Patent WO02053773.  
ACCESSION AX470469  
VERSION AX470469.1 GI:22205594  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 46 11-JUL-2002;  
HENKEL KGAA (DE)  
FEATURES Location/Qualifiers  
source 1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
y 21 AGTCCAGG 28  
|||||  
b 10 AGTCCAGG 3  
RESULT 210  
AX470788  
LOCUS AX470788 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 365 from Patent WO02053773.  
ACCESSION AX470788  
VERSION AX470788.1 GI:22205913  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 365 11-JUL-2002;  
HENKEL KGAA (DE)  
FEATURES Location/Qualifiers  
source 1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
y 19 GGAGTCCA 26  
|||||  
b 2 GGAGTCCA 9  
RESULT 211  
AX470933/c  
LOCUS AX470933 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 510 from Patent WO02053773.  
ACCESSION AX470933  
VERSION AX470933.1 GI:22206058  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 510 11-JUL-2002;  
HENKEL KGAA (DE)  
FEATURES Location/Qualifiers  
source 1..11  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

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Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

20 GAGTCCAG 27
|||||
11 GAGTCCAG 4

SULT 212
471363
CUS AX471363 11 bp DNA linear PAT 09-AUG-2002
FINITION Sequence 940 from Patent WO02053773.
CESSION AX471363
RSION AX471363.1 GI:22206488
YWORDS
URCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 940 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

18 GGGAGTCC 25
|||||
4 GGGAGTCC 11

SULT 213
471851
CUS AX471851 11 bp DNA linear PAT 09-AUG-2002
FINITION Sequence 1428 from Patent WO02053773.
CESSION AX471851
RSION AX471851.1 GI:22206976
YWORDS
URCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 1428 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 GGAGTCCA 26
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3 GGAGTCCA 10

SULT 214
4623060

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LOCUS AX623060 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 101 from Patent WO02053774.
ACCESSION AX623060
VERSION AX623060.1 GI:28451001
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 101 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAG 22
|||||
Db 2 ACAGGGAG 9

RESULT 215
AX623555/c
LOCUS AX623555 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 596 from Patent WO02053774.
ACCESSION AX623555
VERSION AX623555.1 GI:28451496
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 596 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AGTCCAGG 28
|||||
Db 11 AGTCCAGG 4

RESULT 216
AX624143
LOCUS AX624143 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1184 from Patent WO02053774.
ACCESSION AX624143
VERSION AX624143.1 GI:28452084
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS

```

```

TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 1184 11-JUL-2002; (DE)
FEATURES   Location/Qualifiers
           source
           1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 12 TGTACAGG 19
b 4 TGTACAGG 11

RESULT 217
X625138/c
OCUS      X625138
DEFINITION Sequence 2179 from Patent WO02053774.
ACCESSION AX625138
VERSION   AX625138.1 GI:28453079
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2179 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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           1..11
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             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 20 GAGTCCAG 27
b 11 GAGTCCAG 4

RESULT 218
X625188/c
OCUS      X625188
DEFINITION Sequence 2229 from Patent WO02053774.
ACCESSION AX625188
VERSION   AX625188.1 GI:28453129
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2229 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
           source
           1..11
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             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTACGTGT 14
Db 11 CTACGTGT 4

RESULT 219
X625450
LOCUS      X625450
DEFINITION Sequence 2491 from Patent WO02053774.
ACCESSION AX625450
VERSION   AX625450.1 GI:28453391
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2491 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCCTACG 11
Db 4 GCCCTACG 11

RESULT 220
X625464/c
LOCUS      X625464
DEFINITION Sequence 2505 from Patent WO02053774.
ACCESSION AX625464
VERSION   AX625464.1 GI:28453405
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2505 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
           source
           1..11
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             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCTA 9
Db 9 GGGCCCTA 2

RESULT 221
X625855
LOCUS      X625855
DEFINITION Sequence 2896 from Patent WO02053774.

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CESSION      AX625855
RSION        AX625855.1  GI:28453893
WORDS        Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2896 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
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             /mol_type="unassigned DNA"
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Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

20 GAGTCCAG 27
|||||
4 GAGTCCAG 11

SULT 222
626664
CUS          AX626664
FINITION     Sequence 3705 from Patent WO02053774.
CESSION      AX626664
RSION        AX626664.1  GI:28454702
WORDS        Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 3705 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
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Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

18 GGGAGTCC 25
|||||
4 GGGAGTCC 11

SULT 223
627013
CUS          AX627013
FINITION     Sequence 4054 from Patent WO02053774.
CESSION      AX627013
RSION        AX627013.1  GI:28455051
WORDS        Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 4054 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
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             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

18 GGGAGTCC 25
|||||
4 GGGAGTCC 11

SULT 224
627782
CUS          AX627782
FINITION     Sequence 4823 from Patent WO02053774.
CESSION      AX627782
RSION        AX627782.1  GI:28455820
WORDS        Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 4823 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
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             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

21 AGTCCAGG 28
|||||
10 AGTCCAGG 3

SULT 225
629261
CUS          AX629261
FINITION     Sequence 6302 from Patent WO02053774.
CESSION      AX629261
RSION        AX629261.1  GI:28457299
WORDS        Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6302 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

21 AGTCCAGG 28
|||||
10 AGTCCAGG 3

SULT 226
629261
CUS          AX629261
FINITION     Sequence 6302 from Patent WO02053774.
CESSION      AX629261
RSION        AX629261.1  GI:28457299
WORDS        Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6302 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
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             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

21 AGTCCAGG 28
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10 AGTCCAGG 3

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source
1. .11
/organism="Homo sapiens"
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Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

12 TGTACAGG 19
|||||
4 TGTACAGG 11

SULT 231
632559/c
CUS AX632559 11 bp DNA linear PAT 21-FEB-2003
FINITION Sequence 9601 from Patent WO02053774.
CESSION AX632559
RSION AX632559.1 GI:28468174
YWORDS
URCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9601 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

20 GAGTCCAG 27
|||||
11 GAGTCCAG 4

SULT 232
632609/c
CUS AX632609 11 bp DNA linear PAT 21-FEB-2003
FINITION Sequence 9651 from Patent WO02053774.
CESSION AX632609
RSION AX632609.1 GI:28468224
YWORDS
URCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9651 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7 CTACGTGT 14
|||||

Db 11 CTACGTGT 4

RESULT 233
AX632794
LOCUS AX632794 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9836 from Patent WO02053774.
ACCESSION AX632794
VERSION AX632794.1 GI:28468409
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9836 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 GGAGTCCA 26
|||||
3 GGAGTCCA 10

Db 3 GGAGTCCA 10

RESULT 234
I11566
LOCUS I11566 12 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 4 from Patent US 5407822.
ACCESSION I11566
VERSION I11566.1 GI:909084
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Leplatois,P., Loison,G., Pessegue,B. and Shire,D.
TITLE Artificial promoter for the expression of proteins in yeast
JOURNAL Patent: US 5407822-A 4 18-APR-1995;
FEATURES
Location/Qualifiers
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGGGCCCT 8
|||||
5 CGGGCCCT 12

Db 5 CGGGCCCT 12

RESULT 235
I14185
LOCUS I14185 12 bp DNA linear PAT 26-SEP-1995
DEFINITION Sequence 17 from patent US 5446138.
ACCESSION I14185
VERSION I14185.1 GI:996608
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)

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AUTHORS      Blaiseu,P.-L., Legoux,R., Leguay,J.-J. and Schneider,M.
TITLE        Recombinant DNA coding for a protein with endochitinase activity
JOURNAL      Patent: US 5446138-A 17 29-AUG-1995;
FEATURES     Location/Qualifiers
source
1..12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGGGCCCT 8
b 5 CGGGCCCT 12

RESULT 236
AX711182
LOCUS          AX711182
DEFINITION    Sequence 15 from patent US 554526.
ACCESSION     12 bp DNA
VERSION       12 bp DNA
KEYWORDS      linear
SOURCE        PAT 07-OCT-1996
ORGANISM      Unknown.
REFERENCE     1 (bases 1 to 12)
AUTHORS      Baxter-Lowe,L.Ann.
TITLE        Method for HLA Typing
JOURNAL      Patent: US 554526-A 15 13-AUG-1996;
FEATURES     Location/Qualifiers
source
1..12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGGGCCCT 8
b 9 CGGGCCCT 2

RESULT 237
AX235321
LOCUS          AX235321
DEFINITION    Sequence 23 from Patent WO0162967.
ACCESSION     12 bp DNA
VERSION       12 bp DNA
KEYWORDS      linear
SOURCE        PAT 11-SEP-2001
ORGANISM      Hordeum vulgare
REFERENCE     1
AUTHORS      Vider,B.Z. and Katzir,N.
TITLE        A method that compares genomic sequences
JOURNAL      Patent: WO 0162967-A 23 30-AUG-2001;
Genena Ltd. (IL); Agricultural Research Organization Neve Ya'ar
Research Center (IL)
FEATURES     Location/Qualifiers
source
1..12
/organism="Hordeum vulgare"
/mol_type="unassigned DNA"
/db_xref="taxon:4513"

Query Match      28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGGGCCCT 8
b 9 CGGGCCCT 2

RESULT 238
AX711182
LOCUS          AX711182
DEFINITION    Sequence 482 from Patent EP1288296.
ACCESSION     17 bp DNA
VERSION       17 bp DNA
KEYWORDS      linear
SOURCE        PAT 11-APR-2003
ORGANISM      Unknown.
REFERENCE     1
AUTHORS      Draper,K.G., Mcswiggen,J.A., Holecsek,J.J., Dudycz,L.W.,
Macejak,D.G. and Mamane,J.A.
TITLE        Method and reagent for inhibiting HBV viral replication
JOURNAL      Patent: EP 1288296-A 482 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES     Location/Qualifiers
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Nucleic acid clone fragments"

Query Match      28.6%; Score 8; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGGGCCCT 8
b 7 CGGGCCCT 14

RESULT 239
AX625951
LOCUS          AX625951
DEFINITION    Sequence 2992 from Patent WO02053774.
ACCESSION     11 bp DNA
VERSION       11 bp DNA
KEYWORDS      linear
SOURCE        PAT 21-FEB-2003
ORGANISM      Homo sapiens (human)
REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2992 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 7 CTACGTGTACA 17
b 1 CTTCTGTACA 11

RESULT 240
AX472098/c
LOCUS          AX472098
DEFINITION    Sequence 89 from Patent WO02053775.
ACCESSION     11 bp DNA
VERSION       11 bp DNA
KEYWORDS      linear
SOURCE        PAT 09-AUG-2002
ORGANISM      Unknown.
REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2992 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 7 CTACGTGTACA 17
b 1 CTTCTGTACA 11

RESULT 240
AX472098/c
LOCUS          AX472098
DEFINITION    Sequence 89 from Patent WO02053775.
ACCESSION     11 bp DNA
VERSION       11 bp DNA
KEYWORDS      linear
SOURCE        PAT 09-AUG-2002
ORGANISM      Unknown.
REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2992 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 7 CTACGTGTACA 17
b 1 CTTCTGTACA 11

```

```

RESULT 241
LOCUS AR301695 11 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 4 from patent US 5474897.
ACCESSION AR301695
VERSION AR301695.1 GI:1251003
KEYWORDS
SOURCE
   Homo sapiens (human)
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 6 CCTACGCTGAC 16
   ||| |||
11 CTTCTCTGTAC 1
   ||| |||

RESULT 242
LOCUS AR301655 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 236 from patent US 6538173.
ACCESSION AR301655
VERSION AR301655.1 GI:31689457
KEYWORDS
SOURCE
   Homo sapiens (human)
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 16 CAGGAGTCCA 26
   ||| |||
1 CAGAGATTCCA 11
   ||| |||

RESULT 243
LOCUS AR301691 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 272 from patent US 6538173.
ACCESSION AR301691
VERSION AR301691.1 GI:31689493
KEYWORDS
SOURCE
   Unknown.
   /organism="unknown"
   /mol_type="genomic DNA"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 18 GGGAGTCCAGG 28
   ||| |||
1 GGGGCCCCAGG 11
   ||| |||

RESULT 244
LOCUS AX470747 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 324 from Patent WO02053773.
ACCESSION AX470747
VERSION AX470747.1 GI:22205872
KEYWORDS
SOURCE
   Homo sapiens (human)
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

REFERENCE
AUTHORS Hofmann,K., Conrad,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 324 11-JUL-2002;
HENSEL KGAA (DE)
FEATURES
   Location/Qualifiers
     source
       1..11
         /organism="Homo sapiens"
         /mol_type="unassigned DNA"
         /db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 16 CAGGAGTCCA 26
   ||| |||
11 CAGAGAGGCCA 1
   ||| |||

RESULT 245
LOCUS AX470906 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 324 from Patent WO02053773.
ACCESSION AX470906
VERSION AX470906.1 GI:22205872
KEYWORDS
SOURCE
   Homo sapiens (human)
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

REFERENCE
AUTHORS Hofmann,K., Conrad,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 324 11-JUL-2002;
HENSEL KGAA (DE)
FEATURES
   Location/Qualifiers
     source
       1..11
         /organism="Homo sapiens"
         /mol_type="unassigned DNA"
         /db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 16 CAGGAGTCCA 26
   ||| |||
11 CAGAGAGGCCA 1
   ||| |||

RESULT 246
LOCUS AX470906 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 324 from Patent WO02053773.
ACCESSION AX470906
VERSION AX470906.1 GI:22205872
KEYWORDS
SOURCE
   Homo sapiens (human)
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

REFERENCE
AUTHORS Hofmann,K., Conrad,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 324 11-JUL-2002;
HENSEL KGAA (DE)
FEATURES
   Location/Qualifiers
     source
       1..11
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         /mol_type="unassigned DNA"
         /db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 16 CAGGAGTCCA 26
   ||| |||
11 CAGAGAGGCCA 1
   ||| |||

```



DEFINITION Sequence 483 from Patent WO02053773.  
ACCESSION AX470906  
VERSION AX470906.1 GI:22206031  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Hofmann,K., Conradt,M. and Petersohn,D.  
AUTHORS Method for determining skin stress or skin ageing in vitro  
TITLE Patent: WO 02053773-A 483 11-JUL-2002;  
JOURNAL HENKEL KGAA (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Y 2 GGGCCCTTGT 12  
b 11 GGGCCCTTGT 1  
RESULT 246  
AX470952/c  
OCUS AX470952 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 529 from Patent WO02053773.  
ACCESSION AX470952  
VERSION AX470952.1 GI:22206077  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Hofmann,K., Conradt,M. and Petersohn,D.  
AUTHORS Method for determining skin stress or skin ageing in vitro  
TITLE Patent: WO 02053773-A 529 11-JUL-2002;  
JOURNAL HENKEL KGAA (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Y 16 CAGGGAGTCCA 26  
b 11 CAGGGAGTCCA 1  
RESULT 247  
AX471524  
OCUS AX471524 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 1101 from Patent WO02053773.  
ACCESSION AX471524  
VERSION AX471524.1 GI:22206649  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Hofmann,K., Conradt,M. and Petersohn,D.  
AUTHORS Method for determining skin stress or skin ageing in vitro  
TITLE Patent: WO 02053773-A 1101 11-JUL-2002;  
JOURNAL HENKEL KGAA (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

JOURNAL Patent: WO 02053773-A 1101 11-JUL-2002;  
HENKEL KGAA (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Y 11 GGTACAGGA 21  
b 1 GGTAAATGA 11  
RESULT 248  
AX471669/c  
LOCUS AX471669 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 1246 from Patent WO02053773.  
ACCESSION AX471669  
VERSION AX471669.1 GI:22206794  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Hofmann,K., Conradt,M. and Petersohn,D.  
AUTHORS Method for determining skin stress or skin ageing in vitro  
TITLE Patent: WO 02053773-A 1246 11-JUL-2002;  
JOURNAL HENKEL KGAA (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Y 18 GGGACTCAGG 28  
b 11 GGGACTCAGG 1  
RESULT 249  
AX471699/c  
LOCUS AX471699 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 1276 from Patent WO02053773.  
ACCESSION AX471699  
VERSION AX471699.1 GI:22206824  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Hofmann,K., Conradt,M. and Petersohn,D.  
AUTHORS Method for determining skin stress or skin ageing in vitro  
TITLE Patent: WO 02053773-A 1276 11-JUL-2002;  
JOURNAL HENKEL KGAA (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Y 18 GGGACTCAGG 28  
b 11 GGGACTCAGG 1

```

VERSION      AX624024.1  GI:28451965
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 1065 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY              18 GGGAGTCCAGG 28
DB              11 GGGATTTCAGG 1

RESULT 253
LOCUS      AX624330/c
DEFINITION Sequence 1371 from Patent WO02053774.
ACCESSION  AX624330
VERSION     AX624330.1  GI:28452271
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 1371 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY              18 GGGAGTCCAGG 28
DB              11 GGGATTTCAGG 1

RESULT 254
LOCUS      AX624837/c
DEFINITION Sequence 1878 from Patent WO02053774.
ACCESSION  AX624837
VERSION     AX624837.1  GI:28452778
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 1878 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY              18 GGGAGTCCAGG 28
DB              11 GGGATTTCAGG 1

RESULT 252
LOCUS      AX624024/c
DEFINITION Sequence 1065 from Patent WO02053774.
ACCESSION  AX624024
VERSION     AX624024.1  GI:28451965
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 1065 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY              18 GGGAGTCCAGG 28
DB              11 GGGATTTCAGG 1

RESULT 251
LOCUS      AX623640/c
DEFINITION Sequence 681 from Patent WO02053774.
ACCESSION  AX623640
VERSION     AX623640.1  GI:28451581
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 681 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY              16 CAGGGAGTCCA 26
DB              11 CGGGAGGCCA 1

RESULT 250
LOCUS      AX623640/c
DEFINITION Sequence 681 from Patent WO02053774.
ACCESSION  AX623640
VERSION     AX623640.1  GI:28451581
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 681 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY              16 CAGGGAGTCCA 26
DB              11 CGGGAGGCCA 1

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FEATURES
  source
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 27.9%; Score 7.8; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 18 GGGAGTCCAGG 28
b 11 GGAATACAGG 1

RESULT 255
LOCUS AX625047/c
DEFINITION Sequence 2088 from Patent WO02053774.
ACCESSION AX625047
VERSION AX625047.1 GI:28452988
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Petersohn,D., Conradt,M. and Hofmann,K.
  METHOD for determining homeostasis of the skin
  TITLE Patent: WO 02053774-A 2088 11-JUL-2002;
  JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 27.9%; Score 7.8; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 18 GGGAGTCCAGG 28
b 11 GGTAGGCAGG 1

RESULT 256
LOCUS AX625403
DEFINITION Sequence 2444 from Patent WO02053774.
ACCESSION AX625403
VERSION AX625403.1 GI:28453344
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Petersohn,D., Conradt,M. and Hofmann,K.
  METHOD for determining homeostasis of the skin
  TITLE Patent: WO 02053774-A 2444 11-JUL-2002;
  JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 27.9%; Score 7.8; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 18 GGGAGTCCAGG 28
b 11 GGTAGGCAGG 1

RESULT 257
LOCUS AX625794
DEFINITION Sequence 2835 from Patent WO02053774.
ACCESSION AX625794
VERSION AX625794.1 GI:28453735
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Petersohn,D., Conradt,M. and Hofmann,K.
  METHOD for determining homeostasis of the skin
  TITLE Patent: WO 02053774-A 2835 11-JUL-2002;
  JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 27.9%; Score 7.8; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 16 CAGGGAGTCCA 26
b 1 CAGGGGGTTCA 11

RESULT 258
LOCUS AX626034/c
DEFINITION Sequence 3075 from Patent WO02053774.
ACCESSION AX626034
VERSION AX626034.1 GI:28454072
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Petersohn,D., Conradt,M. and Hofmann,K.
  METHOD for determining homeostasis of the skin
  TITLE Patent: WO 02053774-A 3075 11-JUL-2002;
  JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Query Match
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  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 16 CAGGGAGTCCA 26
b 11 CAGAGAGGCCA 1

RESULT 259
LOCUS AX626752/c
DEFINITION Sequence 3793 from Patent WO02053774.
ACCESSION AX626752
VERSION AX626752.1 GI:28454790
KEYWORDS

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Db
  1 AGGGAGACCTG 11

RESULT 257
LOCUS AX625794
DEFINITION Sequence 2835 from Patent WO02053774.
ACCESSION AX625794
VERSION AX625794.1 GI:28453735
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Petersohn,D., Conradt,M. and Hofmann,K.
  METHOD for determining homeostasis of the skin
  TITLE Patent: WO 02053774-A 2835 11-JUL-2002;
  JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
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  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 16 CAGGGAGTCCA 26
b 1 CAGGGGGTTCA 11

RESULT 258
LOCUS AX626034/c
DEFINITION Sequence 3075 from Patent WO02053774.
ACCESSION AX626034
VERSION AX626034.1 GI:28454072
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Petersohn,D., Conradt,M. and Hofmann,K.
  METHOD for determining homeostasis of the skin
  TITLE Patent: WO 02053774-A 3075 11-JUL-2002;
  JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 27.9%; Score 7.8; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 16 CAGGGAGTCCA 26
b 11 CAGAGAGGCCA 1

RESULT 259
LOCUS AX626752/c
DEFINITION Sequence 3793 from Patent WO02053774.
ACCESSION AX626752
VERSION AX626752.1 GI:28454790
KEYWORDS

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URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3793 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
          source
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

          2 GGGCCCTACGT 12
          |||||
          11 GGGCCCTTGT 1

RESULT 260
LOCUS      AX626783              11 bp      DNA              linear      PAT 21-FEB-2003
DEFINITION Sequence 3824 from Patent WO02053774.
ACCESSION  AX626783
VERSION    AX626783.1 GI:28454821
KEYWORDS   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3824 11-JUL-2002; (DE)
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

          18 GGGAGTCCAGG 28
          |||||
          11 GGGGTTCCAGG 1

RESULT 261
LOCUS      AX626888              11 bp      DNA              linear      PAT 21-FEB-2003
DEFINITION Sequence 3929 from Patent WO02053774.
ACCESSION  AX626888
VERSION    AX626888.1 GI:28454926
KEYWORDS   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3929 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3793 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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              /mol_type="unassigned DNA"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

          14 TACAGGAGTC 24
          |||||
          1 TAATGGAGTC 11

RESULT 262
LOCUS      AX627660              11 bp      DNA              linear      PAT 21-FEB-2003
DEFINITION Sequence 4701 from Patent WO02053774.
ACCESSION  AX627660
VERSION    AX627660.1 GI:28455698
KEYWORDS   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 4701 11-JUL-2002; (DE)
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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              /db_xref="taxon:9606"

Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

          16 CAGGGAGTCCA 26
          |||||
          1 CAGTGATCCA 11

RESULT 263
LOCUS      AX627965              11 bp      DNA              linear      PAT 21-FEB-2003
DEFINITION Sequence 5006 from Patent WO02053774.
ACCESSION  AX627965
VERSION    AX627965.1 GI:28456003
KEYWORDS   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 5006 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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              /db_xref="taxon:9606"

Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

          11 GTGTACAGGA 21
          |||||
          1 GTGTAATGGA 11

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RESULT 264
X628121/c
OCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
JOURNAL
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1. .11
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 18 GGGAGTCCAGG 28
|||||
b 11 GGGACTGCAGG 1

RESULT 265
X628521/c
OCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
JOURNAL
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source
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Query Match
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Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 18 GGGAGTCCAGG 28
|||||
b 11 GGGACTGCAGG 1

RESULT 266
X628699/c
OCUS
DEFINITION
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KEYWORDS
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JOURNAL
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Query Match
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Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 17 AGGAGTCCAG 27
|||||
b 11 AGGGAATCTAG 1

RESULT 267
X629205
OCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
JOURNAL
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 16 CAGGAGTCCA 26
|||||
b 11 CGGGGGGTCCA 1

RESULT 268
X629571
OCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
JOURNAL
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 15 ACAGGAGTCC 25
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b 1 ACAGGGTGACC 11

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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 5740 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 16 CAGGAGTCCA 26
|||||
b 11 CGGGGGGTCCA 1

RESULT 267
X629205
OCUS
DEFINITION
ACCESSION
VERSION
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source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 6246 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 15 ACAGGAGTCC 25
|||||
b 1 ACAGGGTGACC 11

RESULT 268
X629571
OCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
JOURNAL
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 6612 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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REFERENCE  
Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE  
METHOD for determining homeostasis of the skin  
JOURNAL  
Patent: WO 02053774-A 8487 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
Location/Qualifiers  
1. .11  
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Query Match 27.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Y 18 GGGAGTCCAGG 28  
|||||  
11 GGGATTCCAGG 1  
b  
RESULT 274  
X631751/c  
OCUS  
DEFINITION  
Sequence 8793 from Patent WO02053774.  
ACCESSION  
X631751  
VERSION  
X631751.1 GI:28459858  
KEYWORDS  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE  
METHOD for determining homeostasis of the skin  
JOURNAL  
Patent: WO 02053774-A 8793 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
Location/Qualifiers  
1. .11  
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/db\_xref="taxon:9606"  
Query Match 27.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Y 18 GGGAGTCCAGG 28  
|||||  
11 GGGATTCCAGG 1  
b  
RESULT 275  
X632258/c  
OCUS  
DEFINITION  
Sequence 9300 from Patent WO02053774.  
ACCESSION  
X632258  
VERSION  
X632258.1 GI:28467873  
KEYWORDS  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE  
METHOD for determining homeostasis of the skin  
JOURNAL  
Patent: WO 02053774-A 9300 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
Location/Qualifiers  
1. .11  
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/mol\_type="unassigned DNA"  
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Query Match 27.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Y 18 GGGAGTCCAGG 28  
|||||  
11 GGGATTCCAGG 1  
b  
RESULT 276  
X632468/c  
LOCUS  
DEFINITION  
Sequence 9510 from Patent WO02053774.  
ACCESSION  
X632468  
VERSION  
X632468.1 GI:28468083  
KEYWORDS  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE  
METHOD for determining homeostasis of the skin  
JOURNAL  
Patent: WO 02053774-A 9510 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
Location/Qualifiers  
1. .11  
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/db\_xref="taxon:9606"  
Query Match 27.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Y 18 GGGAGTCCAGG 28  
|||||  
11 GGGATTCCAGG 1  
b  
RESULT 277  
BD124405  
LOCUS  
DEFINITION  
Compositions and method for healing wound.  
ACCESSION  
BD124405  
VERSION  
BD124405.1 GI:23219350  
KEYWORDS  
JP 2002503460-A/236.  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
Katz,E.H.  
AUTHORS  
TITLE  
Compositions and method for healing wound  
JOURNAL  
Patent: JP 2002503460-A 236 05-FEB-2002;  
THE WISTAR INSTITUTE  
COMMENT  
OS Mus musculus (mouse)  
PN JP 2002503460-A/236  
PD 05-FEB-2002  
PF 13-FEB-1999 JP 2000531545  
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR  
28-SEP-1998 US 60/102051  
PI ELLEN HEBER KATZ  
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC  
C12N5/00  
CC Compositions and method for healing wound  
FH Key Location/Qualifiers  
FT source 1. .11  
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/mol\_type="genomic DNA"  
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source  
1. .11  
Location/Qualifiers  
/organism="Mus musculus (mouse)".

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/db_xref=taxon:10090"

Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

18 GGGAGTCCAGG 28
   |||||
1 GGGGCCCCAGG 11

SULT 278
124441/c
CUS      BD124441      11 bp      DNA      linear      PAT 18-SEP-2002
FINITION Compositions and method for healing wound.
CESSION   BD124441
RSION     BD124441.1 GI:23219386
WORDS     JP 2002503460-A/272.
URCE      Mus musculus
ORGANISM  Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     1 (bases 1 to 11)
JOURNAL   Katz, E.H.
COMMENT   Compositions and method for healing wound
PATENT: JP 2002503460-A 272 05-FEB-2002;
THE WISTAR INSTITUTE
OS Mus musculus (mouse)
PN JP 2002503460-A/272
PD 05-FEB-2002
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key 1..11
FT source Location/Qualifiers
FT /organism="Mus musculus (mouse)".

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Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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   |||||
11 CTTGTAGAGG 1

SULT 279
17665/c
CUS      A47665      12 bp      DNA      linear      PAT 07-MAR-1997
FINITION Sequence 25 from Patent EP0692535.
CESSION   A47665
RSION     A47665.1 GI:2301606
WORDS     unidentified
URCE      unidentified
ORGANISM  unidentified
REFERENCE Colote,S. and Pirotsky,E.
AUTHORS   1 (bases 1 to 12)
TITLE     Oligonucleotides to inhibit the role of isoprenyl protein
JOURNAL   Patent: EP 0692535-A 25 17-JAN-1996;
SOD CONSEILS RECH APPLIC (FR)
Other publication CN 1124142 960612
COMMENT   Other publication CZ 9501688 960515

/db_xref=taxon:10090"

Other publication BR 9503015 960604
Other publication NZ 272398 960426
Other publication HU 72133 960328
Other publication JP 8051385 960227
Other publication FR 2721930 960105
Other publication FR 2721827 960105
Other publication FI 953170 951230
Other publication SE 9502259 951230
Other publication PL 309384 960108
Other publication NO 952601 960102
Other publication AU 2329995 960111
Other publication CA 2152233 951230
Other publication GB 2290791 960110.

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/mol_type="unassigned DNA"
/db_xref=taxon:32644"

Query Match      27.9%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13 GTACAGGAGT 23
       |||||
DB      11 GTCCAGAGAGT 1

RESULT 280
A91496/c
LOCUS     A91496      12 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 23 from Patent WO9824928.
ACCESSION A91496
VERSION   A91496.1 GI:6740451
KEYWORDS  .
SOURCE    unidentified
ORGANISM  unidentified
REFERENCE 1 (bases 1 to 12)
AUTHORS   PALLISGAARD,N. and Hokland,P.
TITLE     DETECTION OF CHROMOSOMAL ABNORMALITIES
JOURNAL   Patent: WO 9824928-A 23 11-JUN-1998;
PALLISGAARD NIELS (DK); HOKLAND PETER (DK)

FEATURES
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/mol_type="unassigned DNA"
/db_xref=taxon:32644"

Query Match      27.9%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 CTACGTGTACA 17
       |||||
DB      11 CTACGGCTACA 1

RESULT 281
AR027883/c
LOCUS     AR027883      12 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 25 from patent US 5856461.
ACCESSION AR027883
VERSION   AR027883.1 GI:5938703
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS   Colote,S. and Pirotsky,E.
TITLE     Oligonucleotides to inhibit the expression of isoprenyl protein
JOURNAL   Patent: US 5856461-A 25 05-JAN-1999;

/db_xref=taxon:10090"
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FEATURES
source
Location/Qualifiers
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/mol_type="unknown"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 13 GTACAGGAGT 23
2 11 GTCCAGAGAGT 1

RESULT 282
LOCUS R167661/c 12 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 25 from patent US 6287769.
ACCESSION AR167661
VERSION AR167661.1 GI:17903456
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Inoue,T.
TITLE Method of amplifying DNA fragment, apparatus for amplifying DNA fragment, method of assaying microorganisms, method of analyzing microorganisms and method of assaying contaminant
JOURNAL Patent: US 6287769-A 25 11-SEP-2001;
FEATURES
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Location/Qualifiers
1..12
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/mol_type="unassigned DNA"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 7 CTACGGTGACA 17
b 11 CTTCTGGTGAGA 1

RESULT 283
LOCUS R167661/c 12 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for amplifying DNA fragment, method for estimating state of microorganism existing and method for estimating state of waste.
ACCESSION E29545
VERSION E29545.1 GI:13021048
KEYWORDS JP 199276176-A 25 12-OCT-1999;
SOURCE JP 199276176-A/25.
ORGANISM unidentified
unclassified.
1 (bases 1 to 12)
Koichi,I.
AUTHORS Method for amplifying DNA fragment, method for estimating state of microorganism existing and method for estimating state of waste
TITLE Patent: JP 199276176-A 25 12-OCT-1999;
JOURNAL SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES
COMMENT OS Unidentified
PN JP 199276176-A/25
PD 12-OCT-1999
PF 31-MAR-1998 JP 1998087652
PR KOICHI INOUE
PI C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
PC C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
Strandedness: Single;
FH Key Location/Qualifiers
FT source 1..12
/organism='Unidentified'.

FEATURES
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Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 7 CTACGGTGACA 17
b 11 CTTCTGGTGAGA 1

RESULT 284
LOCUS E38651/c 12 bp DNA linear PAT 31-JAN-2002
DEFINITION Method and device for amplifying DNA fragment.
ACCESSION E38651
VERSION E38651.1 GI:18621313
KEYWORDS JP 2000270867-A/25.
SOURCE unidentified
unclassified.
ORGANISM unidentified
1 (bases 1 to 12)
Inoue,K.
AUTHORS Method and device for amplifying DNA fragment
TITLE Patent: JP 2000270867-A 25 03-OCT-2000;
JOURNAL SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES
COMMENT OS Unidentified
PN JP 2000270867-A/25
PD 03-OCT-2000
PF 13-MAR-1999 JP 1999076844
PR KOICHI INOUE
PI C12N15/09,C12M1/00,C12Q1/68,C12N15/00
PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..12
/organism='Unidentified'.

FEATURES
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Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 7 CTACGGTGACA 17
b 11 CTTCTGGTGAGA 1

RESULT 285
LOCUS E64077/c 12 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for amplifying DNA fragment, amplification apparatus of DNA fragment, method for assaying a group of microorganisms, method for analyzing a group of microorganisms, and method for assaying contaminating substance.
ACCESSION E64077
VERSION E64077.1 GI:13019481
KEYWORDS JP 199341989-A/25.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Koichi,I.

```

TITLE Method for amplifying DNA fragment, amplification apparatus of DNA fragment, method for assaying a group of microorganisms, method for analyzing a group of microorganisms, and method for assaying contaminating substance  
 JOURNAL Patent: JP 199341983-A 25 14-DEC-1999;  
 SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY AND FISHERIES  
 INVENTOR OS Artificial Sequence  
 PN JP 199341983-A/25  
 PD 14-DEC-1999  
 PR 16-MAR-1999 JP 1993069694  
 PI KOICHI INOUE  
 PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00  
 CC  
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 FT source 1..12  
 FT Location/Qualifiers  
 FT 1..12 /organism="Artificial Sequence".  
 FT 1..12 /organism="synthetic construct"  
 FT /mol\_type="genomic DNA"  
 FT /db\_xref="taxon:32630"  
 Query Match 27.9%; Score 7.8; DB 1; Length 12;  
 Best Local Similarity 81.8%; Pred. No. 1.7e+02;  
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 7 CTACGGTGACA 17  
 11 CTTGCTGTAGA 1  
 SULT 286  
 3754/c  
 CUS 12 bp DNA linear PAT 07-OCT-1996  
 FINITION Sequence 19 from patent US 5538844.  
 I23754  
 CESSION  
 I23754.1 GI:1603624  
 YWORDS  
 URCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 12)  
 AUTHORS Duyao,M.P., MacDonald,M.E. and Gusella,J.F.  
 TITLE Transport protein gene from the Huntington's disease region  
 JOURNAL Patent: US 5538844-A 19 23-JUL-1996;  
 ATURES Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 Query Match 27.9%; Score 7.8; DB 1; Length 12;  
 Best Local Similarity 81.8%; Pred. No. 1.7e+02;  
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 5 CCTACCTGTGA 15  
 12 CCTACCTGAA 2  
 SULT 287  
 15021/c  
 CUS 12 bp DNA linear PAT 13-MAY-1997  
 FINITION Sequence 107 from patent US 5599704.  
 I35021  
 CESSION  
 I35021.1 GI:2087989  
 YWORDS  
 URCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 12)  
 AUTHORS Thompson,J.D. and Draper,K.G.

TITLE ErbB2/neu targeted ribozymes  
 JOURNAL Patent: US 5599704-A 107 04-FEB-1997;  
 FEATURES Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
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 4 GCCCTACGTGT 14  
 12 GCCGTAGGTGT 2  
 RESULT 288  
 AR224412  
 LOCUS 12 bp RNA linear PAT 26-SEP-2002  
 DEFINITION Sequence 9 from patent US 6440723.  
 ACCESSION AR224412  
 VERSION AR224412.1 GI:23333191  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 12)  
 AUTHORS Dale,R.M.K.  
 TITLE Arrays with modified oligonucleotide and polynucleotide compositions  
 JOURNAL Patent: US 6440723-A 9 27-AUG-2002;  
 FEATURES Location/Qualifiers  
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 /organism="unknown"  
 /mol\_type="unassigned RNA"  
 Query Match 27.9%; Score 7.8; DB 1; Length 12;  
 Best Local Similarity 81.8%; Pred. No. 1.7e+02;  
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 15 ACAGGGAGTCC 25  
 1 ATAGGGATCC 11  
 RESULT 289  
 AX073604/c  
 LOCUS 12 bp DNA linear PAT 06-FEB-2001  
 DEFINITION Sequence 26 from Patent WO0104320.  
 ACCESSION AX073604  
 VERSION AX073604.1 GI:12710027  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS Schmidt,A.C., Skiadopoulos,M.H., Collins,P.L., Murphy,B.R., Bailly,J.E. and Durbin,A.P.  
 TITLE Attenuated human-bovine chimeric parainfluenza virus (piv) vaccines  
 JOURNAL Patent: WO 0104320-A 26 18-JAN-2001;  
 THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)  
 FEATURES Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Sequence flanking site for introduction of Bsi WI site for rHPV3 s"  
 Query Match 27.9%; Score 7.8; DB 1; Length 12;  
 Best Local Similarity 81.8%; Pred. No. 1.7e+02;  
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 5 CCCTACGTGTA 15  
| | | | |  
b 11 CCGTACGTCTA 1

RESULT 290  
AX073609/c  
LOCUS AX073609 12 bp DNA linear PAT 06-FEB-2001  
DEFINITION Sequence 31 from Patent WO0104320.  
ACCESSION AX073609  
VERSION AX073609.1 GI:12710032  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Schmidt,A.C., Skiadopoulos,M.H., Collins,P.L., Murphy,B.R.,  
Bailly,J.E. and Durbin,A.P.  
TITLE Attenuated human-bovine chimeric parainfluenza virus (piv) vaccines  
JOURNAL Patent: WO 0104320-A 31 18-JAN-2001;  
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)  
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/db\_xref="taxon:32630"  
/note="Sequence flanking Bsi W1 site in rBPIV3 of sFHNH"

Query Match 27.9%; Score 7.8; DB 1; Length 12;  
Best Local Similarity 81.8%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 5 CCCTACGTGTA 15  
| | | | |  
b 11 CCGTACGTCTA 1

RESULT 291  
AX105625  
LOCUS AX105625 12 bp DNA linear PAT 30-APR-2001  
DEFINITION Sequence 9 from Patent WO013620.  
ACCESSION AX105625  
VERSION AX105625.1 GI:13921655  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Dale,R.M.  
TITLE Arrays with modified oligonucleotide and polynucleotide  
JOURNAL compositions  
Patent: WO 0123620-A 9 05-APR-2001;  
Oligos Etc. Inc. (US)  
FEATURES  
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1. .12  
/organism="synthetic construct"  
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/db\_xref="taxon:32630"  
/note="synthesized oligonucleotide"

Query Match 27.9%; Score 7.8; DB 1; Length 12;  
Best Local Similarity 81.8%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 15 ACAGGAGTCC 25  
| | | | |  
b 1 ATAGGGAATCC 11

RESULT 292  
AX454105/c  
LOCUS AX454105 12 bp DNA linear PAT 06-JUL-2002  
DEFINITION Sequence 55 from Patent WO0202605.

ACCESSION AX454105  
VERSION AX454105.1 GI:21713743  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Skiadopoulos,M.H., Collins,P.L., Murphy,B.R. and Schmidt,A.C.  
TITLE Attenuated human-bovine chimeric parainfluenza virus (piv) vaccines  
JOURNAL Patent: WO 0202605-A 55 10-JAN-2002;  
THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)  
FEATURES  
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1. .12  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Parainfluenza Virus"

Query Match 27.9%; Score 7.8; DB 1; Length 12;  
Best Local Similarity 81.8%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 5 CCCTACGTGTA 15  
| | | | |  
b 11 CCGTACGTCTA 1

RESULT 293  
AX454110/c  
LOCUS AX454110 12 bp DNA linear PAT 06-JUL-2002  
DEFINITION Sequence 60 from Patent WO0202605.  
ACCESSION AX454110  
VERSION AX454110.1 GI:21713748  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Skiadopoulos,M.H., Collins,P.L., Murphy,B.R. and Schmidt,A.C.  
TITLE Attenuated human-bovine chimeric parainfluenza virus (piv) vaccines  
JOURNAL Patent: WO 0202605-A 60 10-JAN-2002;  
THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)  
FEATURES  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Parainfluenza Virus"

Query Match 27.9%; Score 7.8; DB 1; Length 12;  
Best Local Similarity 81.8%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 5 CCCTACGTGTA 15  
| | | | |  
b 11 CCGTACGTCTA 1

RESULT 294  
BD023278/c  
LOCUS BD023278 12 bp DNA linear PAT 27-AUG-2002  
DEFINITION Method for detecting abnormality in chromosome.  
ACCESSION BD023278  
VERSION BD023278.1 GI:22564501  
KEYWORDS JP 2001505428-A/23.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Parigard,N. and Hukurando,P.  
TITLE Method for detecting abnormality in chromosome  
JOURNAL Patent: JP 2001505428-A 23 24-APR-2001;

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COMMENT
PN JP 2001505428-A/23
PD 24-APR-2001
PF 08-DEC-1997 JP 1998525090
PI NEILLIS PARIGARD,PATER HOKURANDO
PC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'DNA (synthetic)';
CC Key Location/Qualifiers.
FH Key Location/Qualifiers
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Query Match 27.9%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

7 CTACGCTGTACA 17
|||||
11 CTACGCTTACA 1

RESULT 295
AX690109/c 25 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 2841 from Patent EPI281758.
ACCESSION AX690109
VERSION AX690109.1 GI:29412967
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2841 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 25;
Best Local Similarity 63.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 296
AX690110/c 25 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 2842 from Patent EPI281758.
ACCESSION AX690110
VERSION AX690110.1 GI:29412968
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2842 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 25;
Best Local Similarity 63.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 297
AX690107/c 25 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 2839 from Patent EPI281758.
ACCESSION AX690107
VERSION AX690107.1 GI:29412965
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2839 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 25;
Best Local Similarity 63.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 298
AX690108/c 25 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 2840 from Patent EPI281758.
ACCESSION AX690108
VERSION AX690108.1 GI:29412966
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2840 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 25;
Best Local Similarity 63.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 299
AX690108/c 25 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 2840 from Patent EPI281758.
ACCESSION AX690108
VERSION AX690108.1 GI:29412966
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2840 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 27.9%; Score 7.8; DB 1; Length 25;
Best Local Similarity 63.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 300
AX690110/c 25 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 2842 from Patent EPI281758.
ACCESSION AX690110
VERSION AX690110.1 GI:29412968
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2842 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 27.9%; Score 7.8; DB 1; Length 25;
Best Local Similarity 63.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 GCCCTACGCTGTACAGGGAG 22
|||||
Db 22 GCACTCGCTGCACACGTAG 4

RESULT 297
AX690107/c 25 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 2839 from Patent EPI281758.
ACCESSION AX690107
VERSION AX690107.1 GI:29412965
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2839 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 25;
Best Local Similarity 63.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 GCCCTACGCTGTACAGGGAG 22
|||||
Db 25 GCACTCGCTGCACACGTAG 7

RESULT 298
AX690108/c 25 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 2840 from Patent EPI281758.
ACCESSION AX690108
VERSION AX690108.1 GI:29412966
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2840 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 25;
Best Local Similarity 63.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 299
AX690108/c 25 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 2840 from Patent EPI281758.
ACCESSION AX690108
VERSION AX690108.1 GI:29412966
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2840 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. .25
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 25;
Best Local Similarity 63.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 300
AX690110/c 25 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 2842 from Patent EPI281758.
ACCESSION AX690110
VERSION AX690110.1 GI:29412968
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2842 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. .25
/organism="Homo sapiens"
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Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 Y 4 GCCTACGTTACAGGAG 22  
 |||||  
 b 24 GCACTCGCTGCACACGTAG 6

RESULT 299  
 X690111/c  
 OCUS AX690111 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 2843 from Patent EP1281758.  
 ACCESSION AX690111  
 CCSSION AX690111  
 ERSION AX690111.1 GI:29412969  
 EYWORDS  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 2843 05-FEB-2003;  
 Aeomica, Inc. (US)  
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 /db\_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 25;  
 Best Local Similarity 53.2%; Pred.No.2.9e+02;  
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Y 4 GCCTACGTTACAGGAG 22  
 |||||  
 b 21 GCACTCGCTGCACACGTAG 3

RESULT 300  
 X690112/c  
 OCUS AX690112 25 bp DNA linear PAT 31-MAR-2003  
 DEFINITION Sequence 2844 from Patent EP1281758.  
 ACCESSION AX690112  
 CCSSION AX690112  
 ERSION AX690112.1 GI:29412970  
 EYWORDS  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
 JOURNAL Patent: EP 1281758-A 2844 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 25;  
 Best Local Similarity 53.2%; Pred.No.2.9e+02;  
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Y 4 GCCTACGTTACAGGAG 22  
 |||||  
 b 20 GCACTCGCTGCACACGTAG 2

RESULT 301  
 X096928/c

LOCUS AX096928 10 bp DNA linear PAT 30-MAR-2001  
 DEFINITION Sequence 2106 from Patent WO0118250.  
 ACCESSION AX096928  
 VERSION AX096928.1 GI:13513196  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and Mccarthy,J.J.  
 TITLE Single nucleotide polymorphisms in genes  
 JOURNAL Patent: WO 0118250-A 2106 15-MAR-2001;  
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)  
 FEATURES  
 Location/Qualifiers  
 1..10  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 27.1%; Score 7.6; DB 1; Length 10;  
 Best Local Similarity 87.5%; Pred.No.1.3e+02;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAG 22  
 :|||||  
 Db 10 MCAGGGAG 3

Search completed: April 19, 2004, 14:25:26  
 Job time : 2 secs

CC skin ageing and/or stress; and identifying or determining the effects of  
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present  
 CC sequence is one of a group of human skin ageing/stress related expressed  
 CC sequence tags (ABQ86246-ABQ87680) of the invention  
 XX  
 SQ Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AGTCCAGG 28  
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 Db 10 AGTCCAGG 3

## RESULT 533

ID ABV68516 standard; cDNA; 11 BP.

XX AC ABV68516;

DT 21-OCT-2002 (first entry)

DE Human skin EST 6302.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

OS Homo sapiens.

XX WO200253774-A2.

PN 11-JUL-2002.

PD 20-DEC-2001; 2001WO-EP015179.

PF 03-JAN-2001; 2001DE-01000127.

XX (HENK ) HENKEL KGAA.

PA Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining  
 PT homeostasis and identifying cosmetic or pharmaceutical agents against  
 PT e.g. skin cancer.

PS Disclosure; Page 200; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed  
 CC in the skin of humans or animals by subjecting a mixture of genetically  
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
 CC so as to identify skin-expressed genes and quantify their expression.  
 CC (M1) is useful for identifying genes involved in skin homeostasis; to  
 CC determine skin homeostasis and to test agent (A) that maintains or  
 CC promotes skin homeostasis or that can be used for treating skin  
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
 CC skin. The present sequence is that of a human expressed sequence tag  
 CC (EST) of the invention

SQ Sequence 11 BP; 2 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAG 22  
 |||||

Db 11 ACAGGGAG 4

## RESULT 534

ABV68894  
 ID ABV68894 standard; cDNA; 11 BP.

XX AC ABV68894;

DT 21-OCT-2002 (first entry)

XX Human skin EST 6680.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

OS Homo sapiens.

XX WO200253774-A2.

PN 11-JUL-2002.

PD 20-DEC-2001; 2001WO-EP015179.

PF 03-JAN-2001; 2001DE-01000127.

XX (HENK ) HENKEL KGAA.

PA Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining  
 PT homeostasis and identifying cosmetic or pharmaceutical agents against  
 PT e.g. skin cancer.

PS Disclosure; Page 211; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed  
 CC in the skin of humans or animals by subjecting a mixture of genetically  
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
 CC so as to identify skin-expressed genes and quantify their expression.  
 CC (M1) is useful for identifying genes involved in skin homeostasis; to  
 CC determine skin homeostasis and to test agent (A) that maintains or  
 CC promotes skin homeostasis or that can be used for treating skin  
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
 CC skin. The present sequence is that of a human expressed sequence tag  
 CC (EST) of the invention

SQ Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCCA 26  
 |||||

Db 2 GGAGTCCA 9

## RESULT 535

ABV70231/c  
 ID ABV70231 standard; cDNA; 11 BP.

XX AC ABV70231;

DT 21-OCT-2002 (first entry)

XX Human skin EST 8017.

DE XX

(HENK ) HENKEL KGAA.  
Petersohn D, Conradt M, Hofmann K;  
WPI; 2002-590638/53.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

IN THE DISTRICT COURT OF THE UNITED STATES FOR THE DISTRICT OF COLUMBIA

WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

homeostasis and iden

e.g. skin cancer.

Claim 24; Page 310; 1345pp; German.

1

The invention relates to in vitro i

encoded factors from skin, to serial analysis of gene expression (SAGE) as well as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention.

used as to identify skin-expressed genes and quantify their expression. (W1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; lichenoid dermatitis; atopic dermatitis; acne; seborrhea; lupus erythematosus; vitiligo; psoriasis; atopic dermatitis; basal cell carcinoma; and sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; atopic dermatitis; acne; seborrhea; lupus erythematosus; lichenosis; ichthyosis; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention.

promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melasma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention.

rosacea; melanoma; basal cell carci

skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

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Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
  28.6%; Score 8; DB 1; Length 11;
  tLocal Similarity 100.0%; Pred No. 2.7e-02;
  ches 8; Conservative 0; Mismatches 0; Indels
  0; Gaps 0;

20 GAGTCCAG 27
  |||||
  11 GAGTCCAG 4

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T 537

315 ABV62315 standard; cDNA; 11 BP.

ARV62315:

21-000-2002 (first entry)

U.S. DEPARTMENT OF COMMERCE  
BUREAU OF ECONOMIC ANALYSIS

human brain est. vol.

Human; skin; dermatological; vulnereary; antipsoriatic; antigeboornader;

psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss. immunosuppressive; antiinflammatory; cytostatic; SAGs; neurodermatitis;

**Homo sapiens.**

WO200253774-A2.

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20-DEC-2001; 2001WO-EP015179.

03-JAN-2001: 2001DE-01000127.

(HENK ) HENKEL KGAA.

Petersohn D, Conradt M, Hofmann K;

WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against

e.g. skin cancer.

Disclosure; Page 28; 1345pp; German.

$$N_{\text{eff}} = 3.36 \times 10^4 \left( \frac{h}{0.7} \right)^2 \left( \frac{\Omega_{\text{eff}}}{0.1} \right) \left( \frac{g_{\text{eff}}}{10.75} \right)^{1/4} \left( \frac{M_{\text{pl}}}{10^{16} \text{ GeV}} \right)^2$$

\_\_\_\_\_

CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 4 A; 2 C; 5 G; 0 T; 0 U; 0 Other;  
  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 15 ACAGGGAG 22  
Db 2 ACAGGGAG 9  
  
RESULT 538  
ABV67037/C  
ID ABV67037 standard; cDNA; 11 BP.  
XX  
AC ABV67037;  
XX  
XX  
DT 21-OCT-2002 (first entry)  
XX  
XX Human skin EST 4823.  
XX  
XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrheic;  
KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200253774-A2.  
XX  
XX 11-JUL-2002.  
XX  
XX 20-DEC-2001; 2001WO-EP015179.  
XX  
XX 03-JAN-2001; 2001DE-01000127.  
XX  
XX (HENK ) HENKEL KGAA.  
XX  
XX Petersohn D, Conradt M, Hofmann K;  
XX  
XX WPI; 2002-590638/63.  
XX  
XX In vitro identification of skin-expressed genes, useful for determining  
XX homeostasis and identifying cosmetic or pharmaceutical agents against  
XX e.g. skin cancer.  
XX  
XX Disclosure; Page 158; 1345pp; German.  
XX  
XX The invention relates to in vitro identification (M1) of genes expressed  
XX in the skin of humans or animals by subjecting a mixture of genetically  
XX encoded factors from skin, to serial analysis of gene expression (SAGE)  
XX so as to identify skin-expressed genes and quantify their expression.  
XX (M1) is useful for identifying genes involved in skin homeostasis; to  
XX determine skin homeostasis and to test agent (A) that maintains or  
XX promotes skin homeostasis or that can be used for treating skin  
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
XX skin. The present sequence is that of a human expressed sequence tag  
XX (EST) of the invention

SQ Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 21 AGTCCAGG 28  
Db 10 AGTCCAGG 3  
  
RESULT 539  
ABV70819  
ID ABV70819 standard; cDNA; 11 BP.  
XX  
AC ABV70819;  
XX  
XX 21-OCT-2002 (first entry)  
XX  
XX Human skin EST 8605.  
XX  
XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrheic;  
KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200253774-A2.  
XX  
XX 11-JUL-2002.  
XX  
XX 20-DEC-2001; 2001WO-EP015179.  
XX  
XX 03-JAN-2001; 2001DE-01000127.  
XX  
XX (HENK ) HENKEL KGAA.  
XX  
XX Petersohn D, Conradt M, Hofmann K;  
XX  
XX WPI; 2002-590638/63.  
XX  
XX In vitro identification of skin-expressed genes, useful for determining  
XX homeostasis and identifying cosmetic or pharmaceutical agents against  
XX e.g. skin cancer.  
XX  
XX Claim 24; Page 275; 1345pp; German.  
XX  
XX The invention relates to in vitro identification (M1) of genes expressed  
XX in the skin of humans or animals by subjecting a mixture of genetically  
XX encoded factors from skin, to serial analysis of gene expression (SAGE)  
XX so as to identify skin-expressed genes and quantify their expression.  
XX (M1) is useful for identifying genes involved in skin homeostasis; to  
XX determine skin homeostasis and to test agent (A) that maintains or  
XX promotes skin homeostasis or that can be used for treating skin  
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
XX skin. The present sequence is that of a human expressed sequence tag  
XX (EST) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 12 TGACAGG 19  
Db 4 TGACAGG 11  
  
RESULT 540  
ABV64705



ID ABV64705 standard; cDNA; 11 BP.  
 XX AC ABV64705;  
 XX DT 21-OCT-2002 (first entry)  
 XX DE Human skin EST 2491.  
 XX XX  
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;  
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
 XX OS Homo sapiens.  
 XX PN WO200253774-A2.  
 XX PD 11-JUL-2002.  
 XX PF 20-DEC-2001; 2001WO-EP015179.  
 XX PR 03-JAN-2001; 2001DE-01000127.  
 XX PA (HENK ) HENKEL KGAA.  
 XX PI Petersohn D, Conradt M, Hofmann K;  
 XX XX WPI; 2002-590638/63.  
 XX PT In vitro identification of skin-expressed genes, useful for determining  
 PT homeostasis and identifying cosmetic or pharmaceutical agents against  
 PT e.g. skin cancer.  
 XX PS Disclosure; Page 94; 1345pp; German.  
 XX XX  
 XX The invention relates to in vitro identification (M1) of genes expressed  
 CC in the skin of humans or animals by subjecting a mixture of genetically  
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
 CC so as to identify skin-expressed genes and quantify their expression.  
 CC (M1) is useful for identifying genes involved in skin homeostasis; to  
 CC determine skin homeostasis and to test agent (A) that maintains or  
 CC promotes skin homeostasis or that can be used for treating skin  
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
 CC skin. The present sequence is that of a human expressed sequence tag  
 CC (EST) of the invention  
 XX SQ Sequence 11 BP; 1 A; 6 C; 3 G; 1 T; 0 U; 0 Other;  
 XX XX  
 XX Query Match 28.6%; Score 8; DB 1; Length 11;  
 XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GCCTACG 11  
 Db 4 GCCTACG 11  
 RESULT 541  
 ID ABV62810 standard; cDNA; 11 BP.  
 XX AC ABV62810;  
 XX DT 21-OCT-2002 (first entry)  
 XX DE Human skin EST 596.  
 XX XX  
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;  
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
 XX OS Homo sapiens.

XX WO200253774-A2.  
 XX 11-JUL-2002.  
 XX 20-DEC-2001; 2001WO-EP015179.  
 XX 03-JAN-2001; 2001DE-01000127.  
 XX (HENK ) HENKEL KGAA.  
 XX Petersohn D, Conradt M, Hofmann K;  
 XX WPI; 2002-590638/63.  
 XX PT In vitro identification of skin-expressed genes, useful for determining  
 PT homeostasis and identifying cosmetic or pharmaceutical agents against  
 PT e.g. skin cancer.  
 XX PS Disclosure; Page 41; 1345pp; German.  
 XX XX  
 XX The invention relates to in vitro identification (M1) of genes expressed  
 CC in the skin of humans or animals by subjecting a mixture of genetically  
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
 CC so as to identify skin-expressed genes and quantify their expression.  
 CC (M1) is useful for identifying genes involved in skin homeostasis; to  
 CC determine skin homeostasis and to test agent (A) that maintains or  
 CC promotes skin homeostasis or that can be used for treating skin  
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
 CC skin. The present sequence is that of a human expressed sequence tag  
 CC (EST) of the invention  
 XX SQ Sequence 11 BP; 1 A; 4 C; 2 G; 4 T; 0 U; 0 Other;  
 XX XX  
 XX Query Match 28.6%; Score 8; DB 1; Length 11;  
 XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 21 AGTCCAGG 28  
 Db 11 AGTCCAGG 4  
 RESULT 542  
 ID ABV64719 standard; cDNA; 11 BP.  
 XX AC ABV64719;  
 XX DT 21-OCT-2002 (first entry)  
 XX DE Human skin EST 2505.  
 XX XX  
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;  
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
 XX OS Homo sapiens.  
 XX PN WO200253774-A2.  
 XX PD 11-JUL-2002.  
 XX PF 20-DEC-2001; 2001WO-EP015179.  
 XX PR 03-JAN-2001; 2001DE-01000127.  
 XX PA (HENK ) HENKEL KGAA.  
 XX PI Petersohn D, Conradt M, Hofmann K;  
 XX XX

DR WPI; 2002-590638/63.  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
XX  
PS Disclosure; Page 94; 1345pp; German.  
XX  
XX The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
XX Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
SQ  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GGGCCCTA 9  
DB 9 GGGCCCTA 2  
RESULT 543  
ABV65110  
ID ABV65110 standard; cDNA; 11 BP.  
XX  
AC ABV65110;  
XX  
XX 21-OCT-2002 (first entry)  
XX Human skin EST 2896.  
XX  
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200253774-A2.  
XX  
XX 11-JUL-2002.  
XX  
XX 20-DEC-2001; 2001WO-EP015179.  
XX  
XX 03-JAN-2001; 2001DE-01000127.  
XX (HENK ) HENKEL KGAA.  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX WPI; 2002-590638/63.  
XX  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
XX Claim 24; Page 312; 1345pp; German.  
XX  
XX The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
XX Sequence 105; 1345pp; German.  
XX  
XX The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to

CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
XX Sequence 11 BP; 3 A; 2 C; 3 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 20 GAGTCCAG 27  
DB 4 GAGTCCAG 11  
RESULT 544  
ABV71864/c  
ID ABV71864 standard; cDNA; 11 BP.  
XX  
AC ABV71864;  
XX  
XX 21-OCT-2002 (first entry)  
XX Human skin EST 9650.  
XX  
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200253774-A2.  
XX  
XX 11-JUL-2002.  
XX  
XX 20-DEC-2001; 2001WO-EP015179.  
XX  
XX 03-JAN-2001; 2001DE-01000127.  
XX (HENK ) HENKEL KGAA.  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX WPI; 2002-590638/63.  
XX  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
XX Claim 24; Page 312; 1345pp; German.  
XX  
XX The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
XX Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 U; 0 Other;  
SQ  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      7 CTACGTGT 14
DB      11 CTACGTGT 4

RESULT 545
ABV65919
ID      ABV65919 standard; cDNA; 11 BP.
XX
AC      ABV65919;
XX
DT      21-OCT-2002 (first entry)
XX
DE      Human skin EST 3705.
XX
KW      Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW      immunosuppressive; antiinflammatory; cycostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS      Homo sapiens.
XX
PN      WO200253774-A2.
XX
PD      11-JUL-2002.
XX
PF      20-DEC-2001; 2001WO-EP015179.
XX
PR      03-JAN-2001; 2001DE-01000127.
XX
PA      (HENK ) HENKEL KGAA.
XX
PI      Petersohn D, Conradt M, Hofmann K;
XX
DR      WPI; 2002-590638/63.
XX
PT      In vitro identification of skin-expressed genes, useful for determining
PT      homeostasis and identifying cosmetic or pharmaceutical agents against
PT      e.g. skin cancer.
XX
PS      Disclosure; Page 128; 1345pp; German.
XX
CC      The invention relates to in vitro identification (M1) of genes expressed
CC      in the skin of humans or animals by subjecting a mixture of genetically
CC      encoded factors from skin, to serial analysis of gene expression (SAGE)
CC      so as to identify skin-expressed genes and quantify their expression.
CC      (M1) is useful for identifying genes involved in skin homeostasis; to
CC      determine skin homeostasis and to test agent (A) that maintains or
CC      promotes skin homeostasis or that can be used for treating skin
CC      disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC      ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC      rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC      skin. The present sequence is that of a human expressed sequence tag
CC      (EST) of the invention
XX
SQ      Sequence 11 BP; 1 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 GGGAGTCC 25
DB      4 GGGAGTCC 11

RESULT 546
ABV63398
ID      ABV63398 standard; cDNA; 11 BP.
XX
AC      ABV63398;
XX
DT      21-OCT-2002 (first entry)
XX

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XX      Human skin EST 1184.
DE
XX      Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW      immunosuppressive; antiinflammatory; cycostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS      Homo sapiens.
XX
PN      WO200253774-A2.
XX
PD      11-JUL-2002.
XX
PF      20-DEC-2001; 2001WO-EP015179.
XX
PR      03-JAN-2001; 2001DE-01000127.
XX
PA      (HENK ) HENKEL KGAA.
XX
PI      Petersohn D, Conradt M, Hofmann K;
XX
DR      WPI; 2002-590638/63.
XX
PT      In vitro identification of skin-expressed genes, useful for determining
PT      homeostasis and identifying cosmetic or pharmaceutical agents against
PT      e.g. skin cancer.
XX
PS      Disclosure; Page 57; 1345pp; German.
XX
CC      The invention relates to in vitro identification (M1) of genes expressed
CC      in the skin of humans or animals by subjecting a mixture of genetically
CC      encoded factors from skin, to serial analysis of gene expression (SAGE)
CC      so as to identify skin-expressed genes and quantify their expression.
CC      (M1) is useful for identifying genes involved in skin homeostasis; to
CC      determine skin homeostasis and to test agent (A) that maintains or
CC      promotes skin homeostasis or that can be used for treating skin
CC      disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC      ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC      rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC      skin. The present sequence is that of a human expressed sequence tag
CC      (EST) of the invention
XX
SQ      Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 TGTACAGG 19
DB      4 TGTACAGG 11

RESULT 547
ABV64393/c
ID      ABV64393 standard; cDNA; 11 BP.
XX
AC      ABV64393;
XX
DT      21-OCT-2002 (first entry)
XX
DE      Human skin EST 2179.
XX
KW      Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW      immunosuppressive; antiinflammatory; cycostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS      Homo sapiens.
XX
PN      WO200253774-A2.
XX
PD      11-JUL-2002.
XX

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PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
XX WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 85; 1345pp; German.  
XX  
XX The invention relates to in vitro identification (M1) of genes expressed  
XX in the skin of humans or animals by subjecting a mixture of genetically  
XX encoded factors from skin, to serial analysis of gene expression (SAGE)  
XX so as to identify skin-expressed genes and quantify their expression.  
XX (M1) is useful for identifying genes involved in skin homeostasis; to  
XX determine skin homeostasis and to test agent (A) that maintains or  
XX promotes skin homeostasis or that can be used for treating skin  
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
XX skin. The present sequence is that of a human expressed sequence tag  
XX (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;  
  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 20 GAGTCCAG 27  
DB 11 GAGTCCAG 4  
|||||  
RESULT 548  
ABV64443/c  
ID ABV64443 standard; cDNA; 11 BP.  
XX  
AC ABV64443;  
XX  
XX 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 2229.  
XX  
XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;  
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
XX (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
XX WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.

XX Disclosure; Page 87; 1345pp; German.  
PS  
XX  
XX The invention relates to in vitro identification (M1) of genes expressed  
XX in the skin of humans or animals by subjecting a mixture of genetically  
XX encoded factors from skin, to serial analysis of gene expression (SAGE)  
XX so as to identify skin-expressed genes and quantify their expression.  
XX (M1) is useful for identifying genes involved in skin homeostasis; to  
XX determine skin homeostasis and to test agent (A) that maintains or  
XX promotes skin homeostasis or that can be used for treating skin  
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
XX skin. The present sequence is that of a human expressed sequence tag  
XX (EST) of the invention  
XX  
SQ Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 U; 0 Other;  
  
Query Match 28.6%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 CTACGTGT 14  
DB 11 CTACGTGT 4  
|||||  
RESULT 549  
ABV72049  
ID ABV72049 standard; cDNA; 11 BP.  
XX  
XX ABV72049;  
AC  
XX 21-OCT-2002 (first entry)  
DT  
XX  
DE Human skin EST 9835.  
XX  
XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;  
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
XX (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
XX WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
XX Claim 24; Page 319; 1345pp; German.  
XX  
XX The invention relates to in vitro identification (M1) of genes expressed  
XX in the skin of humans or animals by subjecting a mixture of genetically  
XX encoded factors from skin, to serial analysis of gene expression (SAGE)  
XX so as to identify skin-expressed genes and quantify their expression.  
XX (M1) is useful for identifying genes involved in skin homeostasis; to  
XX determine skin homeostasis and to test agent (A) that maintains or  
XX promotes skin homeostasis or that can be used for treating skin  
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
XX skin.

CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
SQ

Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCCA 26  
Db 3 GGAGTCCA 10

RESULT 550  
ABV69736  
ID ABV69736 standard; cDNA; 11 BP.  
XX  
AC ABV69736;  
XX  
XX 21-OCT-2002 (first entry)  
XX Human skin EST 7522.  
XX  
XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200253774-A2.  
XX  
XX PD 11-JUL-2002.  
XX  
XX PF 20-DEC-2001; 2001WO-EP015179.  
XX  
XX PR 03-JAN-2001; 2001DE-01000127.  
XX (HENK ) HENKEL KGAA.  
XX PA  
XX PI Petersohn D, Conradt M, Hofmann K;  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200253774-A2.  
XX  
XX PD 11-JUL-2002.  
XX  
XX PF 20-DEC-2001; 2001WO-EP015179.  
XX  
XX PR 03-JAN-2001; 2001DE-01000127.  
XX (HENK ) HENKEL KGAA.  
XX PA  
XX PI Petersohn D, Conradt M, Hofmann K;  
XX  
XX DR WPI; 2002-590638/63.  
XX  
XX PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
XX PS Claim 24; Page 237; 1345pp; German.  
XX  
XX CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE).  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
XX SQ Sequence 11 BP; 4 A; 2 C; 5 G; 0 T; 0 U; 0 Other;  
XX

Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAG 22  
Db 2 ACAGGGAG 9

RESULT 551  
ABV6268  
ID ABV6268 standard; cDNA; 11 BP.  
XX  
AC ABV6268;  
XX  
XX 21-OCT-2002 (first entry)  
XX Human skin EST 4054.  
XX  
XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200253774-A2.  
XX  
XX PD 11-JUL-2002.  
XX  
XX PF 20-DEC-2001; 2001WO-EP015179.  
XX  
XX PR 03-JAN-2001; 2001DE-01000127.  
XX (HENK ) HENKEL KGAA.  
XX PA  
XX PI Petersohn D, Conradt M, Hofmann K;  
XX  
XX DR WPI; 2002-590638/63.  
XX  
XX PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
XX PS Disclosure; Page 137; 1345pp; German.  
XX  
XX CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE).  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
XX SQ Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
XX

Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCTA 9  
Db 3 GGGCCCTA 10

RESULT 552  
ABV68998/c  
ID ABV68998 standard; cDNA; 11 BP.  
XX  
AC ABV68998;  
XX  
XX 21-OCT-2002 (first entry)  
XX Human skin EST 6784.  
XX  
XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;

KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX Homo sapiens.  
XX WO200253774-A2.  
XX 11-JUL-2002.  
XX  
XX 20-DEC-2001; 2001WO-EP015179.  
XX  
XX 03-JAN-2001; 2001DB-01000127.  
XX  
XX (HENK ) HENKEL KGAA.  
XX  
XX Petersohn D, Conradt M, Hofmann K;  
XX WPI; 2002-590638/63.  
XX  
XX In vitro identification of skin-expressed genes, useful for determining  
XX homeostasis and identifying cosmetic or pharmaceutical agents against  
XX e.g. skin cancer.  
XX  
XX Disclosure; Page 213; 1345pp; German.  
XX  
XX The invention relates to in vitro identification (M1) of genes expressed  
XX in the skin of humans or animals by subjecting a mixture of genetically  
XX encoded factors from skin, to serial analysis of gene expression (SAGE)  
XX so as to identify skin-expressed genes and quantify their expression.  
XX (M1) is useful for identifying genes involved in skin homeostasis; to  
XX determine skin homeostasis and to test agent (A) that maintains or  
XX promotes skin homeostasis or that can be used for treating skin  
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
XX skin. The present sequence is that of a human expressed sequence tag  
XX (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 20 GAGTCCAG 27  
Db 9 GAGTCCAG 2  
|||||||  
  
RESULT 553  
ABL91942  
ID ABL91942 standard; cDNA; 11 BP.  
XX  
XX ABL91942;  
XX  
XX 30-MAY-2002 (first entry)  
XX  
XX Human Pan-Endothelial Marker SEQ ID NO 40.  
XX  
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
XX normal endothelial marker; pan-endothelial marker; immunostimulant;  
XX antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
XX polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
XX psoriasis; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200210217-A2.  
XX  
XX 07-FEB-2002.  
XX  
XX 01-AUG-2001; 2001WO-US024031.  
XX  
XX 02-AUG-2000; 2000US-0222599P.

PR 11-AUG-2000; 2000US-0224360P.  
PR 11-APR-2001; 2001US-0282850P.  
XX  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX St Croix B, Kinzler KW, Vogelstein B;  
XX WPI; 2002-291856/33.  
XX  
XX An isolated molecule comprising an antibody variable region which  
XX specifically binds to an extracellular domain of a tumor endothelial  
XX marker (TEM) protein, useful for inhibiting tumor growth.  
XX  
XX Example 4; Page 325; 331pp; English.  
XX  
XX The invention relates to an isolated molecule comprising an antibody  
XX variable region which specifically binds to an extracellular domain of a  
XX tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
XX ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
XX proteins have cytostatic, immunostimulant and antiangiogenic activity.  
XX They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
XX bearing a vascularised tumour, polycystic kidney disease, diabetic  
XX retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
XX genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
XX are disclosed, as are marker oligonucleotide sequences: tumour  
XX endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
XX endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
XX (PEM) ABL91903-ABL91995. The present sequence is that of an  
XX oligonucleotide marker useful to the invention  
XX  
SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;  
  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 GGCCTAC 10  
Db 1 GGCCTAC 8  
|||||||  
  
RESULT 554  
ABK68760/C  
ID ABK68760 standard; DNA; 11 BP.  
XX  
XX ABK68760;  
XX  
XX 02-JUL-2002 (first entry)  
XX  
XX Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.  
XX Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4;  
XX ss.  
XX Homo sapiens.  
XX  
XX WO200218641-A2.  
XX  
XX 07-MAR-2002.  
XX  
XX 30-AUG-2001; 2001WO-IB001580.  
XX  
XX 30-AUG-2000; 2000GB-00021286.  
XX  
XX (GEMI-) GEMINI GENOMICS PLC.  
XX  
XX Risinger C, Andersson MK, Lewander T, Olaiasson E;  
XX WPI; 2002-351712/38.  
XX  
XX Novel primer pairs and sequence determination oligonucleotides useful for  
XX amplifying and detecting novel single nucleotide polymorphisms in the 5'  
XX flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes



RESULT 557  
ABX71867  
ID ABX71867 standard; DNA; 11 BP.  
XX AC ABX71867;  
XX DT 12-MAR-2003 (first entry)  
XX DE DNA tag used to identify human gene encoding PEM 40.  
XX KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
KW Tumour endothelial marker; normal endothelial marker; PEM;  
KW Pan-endothelial marker; polycystic kidney disease; psoriasis;  
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
KW neovascularization; immune response; cytostatic; antidiabetic;  
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.  
XX OS Homo sapiens.  
XX PN WO200283874-A2.  
XX PD 24-OCT-2002.  
XX PF 10-APR-2002; 2002WO-US008253.  
XX PR 11-APR-2001; 2001US-0282850P.  
XX PS 06-FEB-2002; 2002US-0354262P.  
XX PA (UJO ) UNIV JOHNS HOPKINS.  
XX PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
XX WIPI; 2003-093016/08.  
XX PT New purified human transmembrane protein, designated as tumor endothelial  
PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,  
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
PT psoriasis.  
XX PS Disclosure; Page 93; 374pp; English.  
XX CC The present invention relates to a novel method for the isolation of  
CC endothelial cells (ECs), and the identification of genes expressed in  
CC normal and tumour ECs. Tumour endothelial marker (TEM), normal  
CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
CC identified in human ECs. The human EC marker proteins and the  
CC polynucleotide sequences encoding them are useful for detecting,  
CC diagnosing or treating tumours as well as polycystic kidney disease,  
CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for  
CC inducing an immune response to tumour endothelial cells in a patient, or  
CC for identifying candidate drugs for treating tumours. ABX71828-ABX71999  
CC represent DNA tags for human PEM, TEM or NEM genes  
XX Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;  
Query Match 28.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GGCCCTAC 10  
Db 1 GGCCCTAC 8  
RESULT 558  
AA79373  
ID AAX79373 standard; DNA; 12 BP.  
XX AC AAX79373;  
XX

DT 17-AUG-1999 (first entry)  
XX HLA-DR typing probe L74.  
XX Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;  
KW major histocompatibility complex; bone marrow transplant; primer;  
KW amplification; polymerase chain reaction; probe; polymorphism;  
KW sequence-specific oligonucleotide probe hybridisation; ss.  
XX OS Synthetic.  
XX PN US5468611-A.  
XX PD 21-NOV-1995.  
XX PF 08-APR-1993; 93US-00045530.  
XX PR 27-JUN-1990; 90US-00544218.  
XX PA (BLOO-) BLOOD CENT RES FOUND INC.  
XX PI Gorski JA, Baxter-Lowe LA;  
XX WIPI; 1996-010091/01.  
XX PT Improved method for HLA typing - by DNA amplification and sequence-  
PT specific oligonucleotide hybridisation, used to select bone marrow  
PT donors.  
XX PS Disclosure; Col 19-20; 20pp; English.  
XX CC A novel method of typing the human leukocyte antigen (HLA) of the major  
CC histocompatibility complex (MHC), esp. for typing donors for bone marrow  
CC transplants, involves determining if the donor tissue HLA-DR alleles are  
CC selected from the gp.: HLA-DRW52C, DR12a.b, DR3a.n, DR5a-e, DRNew1, DR6a,  
CC DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and DR1a-  
CC c. The method uses PCR to amplify these regions followed by sequence-  
CC specific oligonucleotide probe hybridisation (SSOPH) using the probes  
CC AAX79365-X79429. SSOPH allows detection of polymorphisms that predict  
CC differences at a single amino acid level thus reducing errors and  
CC improving the chance of successfully matching tissues  
XX Sequence 12 BP; 1 A; 4 C; 6 G; 1 T; 0 U; 0 Other;  
Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGGCCCT 8  
Db 4 CGGGCCCT 11  
RESULT 559  
AA741818/c  
ID AAT41818 standard; DNA; 12 BP.  
XX AC AAT41818;  
XX DT 25-MAR-2003 (revised)  
XX DT 18-DEC-1996 (first entry)  
XX DE HLA allele, HLA-DRB1\*08, \*12 and \*1404 resolution probe, L74.  
XX KW Human leukocyte antigen; HLA; allele; HLA-DR\*08; HLA-DR\*12; locus B1;  
KW polymorphism; amplify; conserved region; detection; primer; probe;  
KW tissue matching; identifying disease susceptibility; ss.  
XX OS Synthetic.  
XX PN US5545526-A.  
XX PS 13-AUG-1996.



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XX PF 01-MAR-1993; 93US-00025039.
XX PD 27-JUN-1990; 90US-00544218.
XX PR (BLOO-) BLOOD CENT RES FOUND INC.
XX PA Baxter-Lowe LA;
XX PI WPI; 1996-383664/38.
XX DR Human leukocyte antigen typing of tissue samples - using allele-specific
XX PT amplification to distinguish allele pairs.
XX PS Example 1; Col 19; 24pp; English.
XX CC The sequences given in AAT1811-20 represent probes which were used to
XX CC resolve the human leukocyte antigen (HLA) DRB1 alleles, DRB1*08, *12 and
XX CC *1404. This probe sequence hybridises to the Leu74 coding region found in
XX CC alleles *0801, *0802, *0803 and 0804. These probes may be used in the
XX CC method of invention which concerns HLA typing of a sample for an unknown
XX CC pair of alleles. The pair of alleles comprises one of two known types
XX CC which have the same overall set of polymorphisms but have a different
XX CC distribution of polymorphisms between their two alleles. The method
XX CC comprises selectively amplifying the DNA of just one allele of the
XX CC unknown pair and analysing the amplified DNA to determine which
XX CC polymorphisms are present in that allele, and therefore assigning the
XX CC unknown pair to the known type having that allele. The method comprises
XX CC three test stages. The first stage is to establish the number of alleles
XX CC present in each sample. Primers corresponding to fairly well conserved
XX CC regions of a locus will increase the likelihood that unknown alleles will
XX CC be amplified and potentially detected by hybridisation with a probe. In
XX CC the second stage, the group or basic type identified determines which set
XX CC of allele specific primers will be used. The first of the two primers
XX CC comprises an opt. labeled sequence common to each allele of the group
XX CC identified in the first stage but different from other groups identified
XX CC in stage one. The second primer may be a mixture of different labeled
XX CC primers, complementary to two or more sequences within the group, or the
XX CC amplification may be performed with only one second primer to detect the
XX CC presence of a single group of alleles. In the third stage the specific
XX CC allele is determined. This may be done by amplification or hybridisation
XX CC using a radiolabelled probe. The method may be used for tissue matching,
XX CC identifying disease susceptibility, etc. The method of the invention esp.
XX CC distinguishes between DQB1*0304/DQB1*0302 and DQB1*0301/DQB1*0302.
XX CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 12 BP; 1 A; 6 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCCT 8
Db 9 CGGGCCCT 2
|||||||

RESULT 560
AAV16569
ID AAV16569 standard; DNA; 12 BP.
XX AC AAV16569;
XX DT 12-JUN-1998 (first entry)
XX DE Probe L74 used to identify HLA-DR sequences.
XX KW DR region; major histocompatibility complex; HLA-DR; HLA-typing;
XX KW HLA-DR beta consensus sequence; allelic polymorphism;
XX KW HLA-DR beta-allelic polymorphism; probe; bone marrow; transplant; ss.
XX OS Synthetic.
XX OS Homo sapiens.

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XX PN US5702885-A.
XX PD 30-DEC-1997.
XX PF 08-APR-1993; 93US-00057957.
XX PR 27-JUN-1990; 90US-00544218.
XX PA (BLOO-) BLOOD CENT RES FOUND INC.
XX PI Gorski JA, Baxter-Lowe LA;
XX DR WPI; 1998-076408/07.
XX PT Oligo:nucleotide probes and primers and methods for HLA typing -
XX PT particularly for tissue typing for bone marrow transplants.
XX PS Disclosure; Col 19; 20pp; English.
XX CC Probes AAV16561-624 are used to identify differences in the DR region of
XX CC human major histocompatibility complex (HLA-DR). The specification
XX CC describes a method for HLA-typing, which includes an oligonucleotide
XX CC probe which undergoes sequence-specific hybridisation with an HLA-DR beta
XX CC consensus sequence at positions 61-84. The probe contains a labelling
XX CC substance other than a nucleotide sequence, which facilitates detection
XX CC of the probe. The HLA sequence of a subject is PCR amplified, and a probe
XX CC that recognises an allelic polymorphism at a selected HLA locus is
XX CC contacted with the amplified product. This first probe recognises a HLA-
XX CC DR beta-allelic polymorphism. A second (different) probe is brought into
XX CC contact with a second sample of the amplified DNA in a separate reaction,
XX CC and hybridisation detected. The probes and primers are used for HLA
XX CC typing, e.g. for tissue, especially bone marrow, transplants
XX SQ Sequence 12 BP; 1 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCCT 8
Db 4 CGGGCCCT 11
|||||||

RESULT 561
ABH93621/C
ID ABH93621 standard; DNA; 12 BP.
XX AC ABH93621;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 293614 for detecting SNP TSC0015707.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPITG-) EPITGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX OS

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DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX  
 BS Claim 1; SEQ ID NO 23614; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABR00010-ABR2073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;  
 Query Match 28.6%; Score 8; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred.No. 3.1e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 TAGCGTGA 15  
 DB 12 TAGCGTGA 5  
 |||||  
 |||||  
 RESULT 562  
 ABI06748/c  
 ID ABI06748 standard; DNA; 12 BP.  
 XX  
 AC ABI06748;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 306721 for detecting SNP TSC0022148.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic;  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 FD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 306721; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABR00010-ABR2073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

QY 5 CCTACGCT 12  
Db 5 CCTACGCT 12  
RESULT 564  
ABI56358  
ID ABI56358 standard; DNA; 12 BP.  
AC ABI56358;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 356331 for detecting SNP TSC0050060.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
DT 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 356331; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 1 C; 3 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 TACGTGTA 15  
Db 1 TACGTGTA 8  
RESULT 565  
ABH70251  
ID ABH70251 standard; DNA; 12 BP.  
XX  
AC ABH70251;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 289277 for detecting SNP TSC0013867.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
DT 18-OCT-2001.  
XX

XX  
DE Oligonucleotide primer SEQ ID NO 270228 for detecting SNP TSC0002052.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
DT 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 270228; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;  
XX  
Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 TACGTGTA 15  
Db 2 TACGTGTA 9  
RESULT 566  
ABH89284  
ID ABH89284 standard; DNA; 12 BP.  
XX  
AC ABH89284;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 289277 for detecting SNP TSC0013867.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
DT 18-OCT-2001.  
XX

PF 06-APR-2001; 2001WO-IB000713.  
XX  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 289277; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 12 BP; 4 A; 1 C; 4 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 TACGTGTA 15  
DB 3 TACGTGTA 10  
|||||||  
RESULT 567  
ABH92486/c  
ID ABH92486 standard; DNA; 12 BP.  
XX  
XX ABH92486;  
AC  
XX  
XX 22-FEB-2002 (first entry)  
DT  
XX  
XX Oligonucleotide primer SEQ ID NO 292479 for detecting SNP TSC0015230.  
DE  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200177384-A2.  
PN  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX Oligonucleotide primer SEQ ID NO 292479 for detecting SNP TSC0015230.  
PF  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200177384-A2.  
PN  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX  
XX  
XX Claim 1; SEQ ID NO 292479; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 12 BP; 1 A; 2 C; 5 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GCCCTACG 11  
DB 10 GCCCTACG 3  
|||||||  
RESULT 568  
AB113410  
ID AB113410 standard; DNA; 12 BP.  
XX  
XX AB113410;  
AC  
XX  
XX 22-FEB-2002 (first entry)  
DT  
XX  
XX Oligonucleotide primer SEQ ID NO 313383 for detecting SNP TSC0025713.  
DE  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200177384-A2.  
PN  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 313383; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX

CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 0 Other;  
  
Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 CCTACGT 12  
DB 5 CCTACGT 12  
|||||||  
|||  
  
RESULT 569  
AB162488  
ID AB162488 standard; DNA; 12 BP.  
XX  
AC AB162488;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 362461 for detecting SNP TSC0053239.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 362461 for detecting SNP TSC0053239.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 362461; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 1 C; 2 G; 5 T; 0 U; 0 Other;  
  
Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 TACGTGTA 15  
DB 4 TACGTGTA 11  
|||||||  
|||

RESULT 570  
AB113984  
ID AB113984 standard; DNA; 12 BP.  
XX  
AC AB113984;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 313957 for detecting SNP TSC0026047.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 313957; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;  
  
Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 TACGTGTA 15  
DB 2 TACGTGTA 9  
|||||||  
|||  
  
RESULT 571  
ABH95542/c  
ID ABH95542 standard; DNA; 12 BP.  
XX  
AC ABH95542;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 295535 for detecting SNP TSC0016627.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPITG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 295535; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 5 CCCTACGT 12  
DB 8 CCCTACGT 1  
RESULT 572  
ABH76707  
ID ABH76707 standard; DNA; 12 BP.  
XX  
XX AC ABH76707;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
XX Oligonucleotide primer SEQ ID NO 276700 for detecting SNP TSC0004266.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPITG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 276700; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 12 BP; 2 A; 1 C; 3 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 8 TACGTGTA 15  
DB 3 TACGTGTA 10  
RESULT 573  
ABI76102/c  
ID ABI76102 standard; DNA; 12 BP.  
XX  
XX AC ABI76102;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
XX Oligonucleotide primer SEQ ID NO 376075 for detecting SNP TSC0061603.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPITG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 376075; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTACGT 12  
DB 10 CCTACGT 3

RESULT 574  
ABH81705  
ID ABH81705 standard; DNA; 12 BP.  
AC ABH81705;  
XX  
XX  
DT 22-FEB-2002 (first entry)  
DE Oligonucleotide primer SEQ ID NO 281698 for detecting SNP TSC0010001.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 281698; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TACGTGTA 15  
DB 5 TACGTGTA 12

RESULT 575  
ABH85829/c  
ID ABH85829 standard; DNA; 12 BP.  
AC ABH85829;  
XX  
XX  
DT 22-FEB-2002 (first entry)  
DE Oligonucleotide primer SEQ ID NO 285822 for detecting SNP TSC0012462.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 285822; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TACGTGTA 15  
DB 10 TACGTGTA 3

RESULT 576  
ABH86354  
ID ABH86354 standard; DNA; 12 BP.  
XX

```

AC ABH86354;
XX
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 286347 for detecting SNP TSC0012678.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 286347; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 1 C; 7 G; 1 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 28.6%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred.No. 3.1e-02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 17 AGGGAGTC 24
DB 5 AGGGAGTC 12
|||||
RESULT 577
ABII3988
ID ABI13988 standard; DNA; 12 BP.
XX
XX ABI13988;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 313961 for detecting SNP TSC0026047.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX

```

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XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 313961; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 28.6%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred.No. 3.1e-02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 8 TACGTGTA 15
DB 2 TACGTGTA 9
|||||
RESULT 578
ABH97060/C
ID ABH97060 standard; DNA; 12 BP.
XX
XX ABH97060;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 297053 for detecting SNP TSC0017414.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX

```



PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 297053; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCTACGCT 12  
 Db 10 CCTACGCT 3  
 |||||

RESULT 579

ABI16213

ID ABI16213 standard; DNA; 12 BP.

XX AC ABI16213;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 316186 for detecting SNP TSC0027326.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WC200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 316186; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 ACGGAGTC 24  
 Db 5 ACGGAGTC 12  
 |||||

RESULT 580

ABI56360

ID ABI56360 standard; DNA; 12 BP.

XX AC ABI56360;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 356333 for detecting SNP TSC0050060.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WC200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 356333; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TACGTGTA 15

```

Db      1 TACGTGTA 8
RESULT 581
ABI28945/C
ID ABI28945 standard; DNA; 12 BP.
XX
AC ABI28945;
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 328918 for detecting SNP TSC0034654.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 328918; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 6 C; 1 G; 3 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 AGGGAGTC 24
Db 11 AGGGAGTC 4
RESULT 582
ABI10703/C
ID ABI10703 standard; DNA; 12 BP.
XX
AC ABI10703;
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 310676 for detecting SNP TSC0024049.
DE

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XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 310676; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TACGTGTA 15
Db 11 TACGTGTA 4
RESULT 583
ABI75403/C
ID ABI75403 standard; DNA; 12 BP.
XX
AC ABI75403;
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 375376 for detecting SNP TSC0061224.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX

```

PR 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
PA Olek A, Piepenbrock C, Berlin K;  
PI WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 375376; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 5 A; 1 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CCCTACGT 12  
DB 9 CCCTACGT 2  
RESULT 584  
ABI63259  
ID ABI63259 standard; DNA; 12 BP.  
XX  
XX  
AC ABI63259;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
XX Oligonucleotide primer SEQ ID NO 363232 for detecting SNP TSC0053719.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
PN  
XX  
PD 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 363232; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;  
Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 TACGTGTA 15  
DB 3 TACGTGTA 10  
RESULT 585  
ABH73580  
ID ABH73580 standard; DNA; 12 BP.  
XX  
XX  
AC ABH73580;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
XX Oligonucleotide primer SEQ ID NO 273565 for detecting SNP TSC0003234.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
PN  
XX  
PD 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 273565; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

```
XX SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TACGTGTA 15
DB 3 TACGTGTA 10

RESULT 586
ABI5650/c
ID ABI56650 standard; DNA; 12 BP.
XX AC ABI56650;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 356623 for detecting SNP TSC0050224.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 356623; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TACGTGTA 15
DB 11 TACGTGTA 4

RESULT 587
```

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ABI59399/c
ID ABI59399 standard; DNA; 12 BP.
XX AC ABI59399;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 359372 for detecting SNP TSC0051583.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 359372; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 2 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TACGTGTA 15
DB 9 TACGTGTA 2

RESULT 588
AAF92629
ID AAF92629 standard; DNA; 12 BP.
XX AC AAF92629;
XX DT 16-MAY-2001 (first entry)
XX DE HLA-DR typing probe #9.
XX KW Human; leukocyte antigen; HLA; typing; sequence specific probe; SSOPH;
XX KW ss.
XX OS Homo sapiens.
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XX US6194147-B1.  
 XX PD 27-FEB-2001.  
 XX PF 30-DEC-1997; 97US-0000805.  
 XX PR 27-JUN-1990; 90US-00544218.  
 XX PR 08-APR-1993; 93US-00057957.  
 XX PA (BLOO-) BLOOD CENT RES FOUND INC.  
 XX PI Baxter-Lowe LA, Gorski JA;  
 XX DR WPI; 2001-217923/22.  
 XX PT Human leukocyte antigen typing by amplifying a sample followed by  
 PT sequence specific oligonucleotide hybridization with labeled  
 PT oligonucleotide probes that hybridize with a series of known control DNA  
 PT sequences.  
 XX PS Disclosure; Col 11-14; 16pp; English.  
 XX CC The present invention relates to human leukocyte antigen (HLA) typing.  
 CC The method involves detecting polymorphic residues by sequence specific  
 CC oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide  
 CC probes  
 XX SQ Sequence 12 BP; 1 A; 4 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 28.6%; Score 8; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CGGGCCCT 8  
 DB 4 CGGGCCCT 11  
 RESULT 589  
 AAF92695  
 ID AAF92695 standard; DNA; 12 BP.  
 XX AC AAF92695;  
 XX DT 16-MAY-2001 (first entry)  
 XX DE HLA-DR allele group typing probe #10.  
 XX KW Human; leukocyte antigen; HLA; typing; sequence specific probe; SSOPH;  
 XX KW ss.  
 XX OS Homo sapiens.  
 XX PN US6194147-B1.  
 XX PD 27-FEB-2001.  
 XX PF 30-DEC-1997; 97US-0000805.  
 XX PR 27-JUN-1990; 90US-00544218.  
 XX PR 08-APR-1993; 93US-00057957.  
 XX PA (BLOO-) BLOOD CENT RES FOUND INC.  
 XX PI Baxter-Lowe LA, Gorski JA;  
 XX DR WPI; 2001-217923/22.  
 XX PT Human leukocyte antigen typing by amplifying a sample followed by  
 PT sequence specific oligonucleotide hybridization with labeled  
 PT oligonucleotide probes that hybridize with a series of known control DNA  
 PT sequences.

XX Disclosure; Col 11-14; 16pp; English.  
 XX PS The present invention relates to human leukocyte antigen (HLA) typing.  
 CC The method involves detecting polymorphic residues by sequence specific  
 CC oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide  
 CC probes  
 XX SQ Sequence 12 BP; 1 A; 4 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 28.6%; Score 8; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CGGGCCCT 8  
 DB 4 CGGGCCCT 11  
 RESULT 590  
 ABL42258  
 ID ABL42258 standard; DNA; 12 BP.  
 XX AC ABL42258;  
 XX DT 01-JUL-2002 (first entry)  
 XX DE Plant cis-regulatory sequence from barley ABA.  
 XX KW DNA fingerprinting; cancer; agriculture; breeding; PCR; primer;  
 KW gene family; ds.  
 XX OS Hordeum sp.  
 XX PN WO200162967-A2.  
 XX PD 30-AUG-2001.  
 XX PF 19-FEB-2001; 2001WO-IL000151.  
 XX PR 22-FEB-2000; 2000IL-00134660.  
 XX PR 02-JUL-2000; 2000IL-00137124.  
 XX PR 20-AUG-2000; 2000IL-00137959.  
 XX PA (GENE-) GENEVA LTD.  
 XX PA (AGRI-) AGRIC RES ORG NEWE YA'AR RES CENTE.  
 XX PI Vidar B, Katzir N;  
 XX WPI; 2002-239525/29.  
 XX PT Polymerase chain reaction based method of DNA fingerprinting, useful for  
 PT analyzing genes, e.g. for identifying genes involved in cancer formation,  
 PT involves using a mix of primers that match the conserved regions of a  
 PT gene family.  
 XX PS Example; Page 17; 28pp; English.  
 XX CC The invention relates to a polymerase chain reaction (PCR) based method  
 CC of DNA fingerprinting, comprising using primers that match the conserved  
 CC regions of a gene family. The method is useful for gene expression  
 CC analysis of any cell or tissue, or for the performance of DNA  
 CC fingerprinting analysis of the same organism in order that one will  
 CC reveal the function of a gene that produced differential product between  
 CC genotypes. The method is also useful for identifying PCR reactions that  
 CC contain a gene of interest in a gene family reverse transcriptase (RT)-  
 CC PCR expression analysis. The method is also useful for identifying genes  
 CC that belong to a gene family that might be involved in cancer formation.  
 CC The method is particularly useful for comparing genomic sequences. These  
 CC are also applicable in agriculture (e.g. to mark useful genes to assist  
 CC breeding). The current sequence represents a plant cis-regulatory  
 CC sequence. This is used in DNA fingerprinting using primers or a mix of  
 CC primers that match the sequence of ubiquitous cis-acting regulatory

CC elements  
 XX Sequence 12 BP; 1 A; 4 C; 5 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 28.6%; Score 8; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCTACGTG 13  
 |||||  
 Db 1 CCTACGTG 8

RESULT 591  
 ABX10158  
 ID ABX10158 standard; cDNA; 12 BP.  
 XX  
 AC ABX10158;  
 XX  
 DT 27-JAN-2003 (first entry)  
 XX Human TIGR/Myocilin variant cDNA deletion 3' flank #1.  
 XX  
 KW Human; ss; TIGR; MYOC; Myocilin; Glaucoma; blindness;  
 KW trabecular meshwork inducible glucocorticoid responsive protein;  
 KW retinal degenerative disease; RDB; retinitis pigmentosa;  
 KW macular degeneration; Usher syndrome; cardiovascular disease;  
 KW congenital heart disease; myocardial ischaemia; stroke;  
 KW acute endocarditis; hypertensive heart disease; arrhythmia;  
 KW arteriosclerotic heart disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200282969-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 11-DEC-2001; 2001WO-US048622.  
 XX  
 PR 05-APR-2001; 2001US-0281442P.  
 PR 23-JUL-2001; 2001US-0306889P.  
 XX  
 PA (KONG/) KONG T H.  
 XX  
 PI Kong TH;  
 XX  
 DR WPI; 2003-058597/05.  
 XX  
 PT Determining the presence or the risk of having glaucoma, retinal  
 PT degenerative or cardiovascular diseases in a subject, comprises  
 PT generating transcriptional or translational profiles based on myocilin  
 PT nucleic acids and proteins.  
 XX  
 PS Disclosure; Fig 4c; 55pp; English.

CC The invention relates to determining whether a subject has or is at risk  
 CC of developing glaucoma, retinal degenerative disease, or a cardiovascular  
 CC disease, comprises generating a transcriptional or translational profile  
 CC (i.e. 'fingerprint') in the subject or in a sample obtained from the  
 CC subject, based on the expression of the different myocilin (MYOC, also  
 CC known as trabecular meshwork inducible glucocorticoid responsive protein,  
 CC TIGR) mRNA species or polypeptide forms, where a difference in the  
 CC profile relative to that in a normal subject indicates that the subject  
 CC has or is at risk of developing the above-mentioned diseases. Also  
 CC included are: (1) a method for establishing MYOC genetic population  
 CC profile in a population of individuals having glaucoma, retinal  
 CC degenerative disease, or a cardiovascular disease; (2) a method for  
 CC pharmacogenomically selecting a therapy to administer to an individual  
 CC having glaucoma, retinal degenerative disease, or a cardiovascular  
 CC disease, comprising determining MYOC genetic profile of an individual and  
 CC comparing the individual's MYOC genetic profile to MYOC genetic  
 CC population profile, to select a therapy for administration to the  
 CC individual; and a kit for determining whether a subject has or is likely

CC to develop glaucoma, retinal degenerative disease, or a cardiovascular  
 CC disease, comprising a probe or primer which hybridises to the MYOC  
 CC nucleic acid, or an antibody or peptide probe capable of specifically  
 CC binding to the novel MYOC polypeptide(s), and instructions for use. The  
 CC method is useful for the prognosis and/or diagnosis of glaucoma, retinal  
 CC degenerative diseases (RDB) or cardiovascular diseases (e.g. blindness,  
 CC retinitis pigmentosa, macular degeneration, Usher syndrome, congenital  
 CC heart disease, myocardial ischaemia, stroke, acute endocarditis,  
 CC hypertensive heart disease, arrhythmia and arteriosclerotic heart  
 CC disease), and in screening assays for the identification of therapeutics  
 CC and the evaluation of their effectiveness for treating the above-  
 CC mentioned diseases in a subject. The present sequence represents the 3'  
 CC flanking sequence surrounding the deletion present in a MYOC cDNA variant  
 XX  
 SQ Sequence 12 BP; 4 A; 3 C; 3 G; 2 T; 0 U; 0 Other;  
 Query Match 28.6%; Score 8; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GAGTCCAG 27  
 |||||  
 Db 2 GAGTCCAG 9

RESULT 592  
 AAX09580/C  
 ID AAX09580 standard; DNA; 15 BP.  
 XX  
 AC AAX09580;  
 XX  
 DT 24-MAR-1999 (first entry)  
 XX  
 DE Human biallelic polymorphic marker upstream primer #460.  
 XX  
 KW Polymorphism; biallelic; human; forensic; paternity testing; disease;  
 KW detection; phenotypic typing; characteristic; infection; hereditary;  
 KW autoimmune disease; cancer; inflammation; drug; therapy; medication;  
 KW treatment; marker; primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9820165-A2.  
 XX  
 PD 14-MAY-1998.  
 XX  
 PF 05-NOV-1997; 97WO-US020313.  
 XX  
 PR 06-NOV-1996; 96US-0030455P.  
 XX  
 PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 XX  
 PI Lander ES, Wang D, Hudson T;  
 XX  
 DR WPI; 1998-286974/25.  
 XX  
 PT New isolated nucleic acid segments from the human genome - used for  
 PT determining polymorphic forms for use in e.g. forensics, paternity  
 PT testing or phenotypic typing for disease.  
 XX  
 PS Claim 15; Page 207; 310pp; English.

CC AAX09121-X10268 are allele-specific oligonucleotide primers used in the  
 CC isolation of various biallelic polymorphic markers found in the human  
 CC genome (represented in AAX10269-X12937). These primers can be used in a  
 CC method for determining polymorphic forms in an individual for use in e.g.  
 CC forensics, paternity testing or for phenotypic typing for diseases such  
 CC as egamaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial  
 CC hypercholesterolemia, polycystic kidney disease, hereditary  
 CC spherocytosis, von Willebrand's disease, tuberosus sclerosis, hereditary  
 CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos



RESULT 595  
 ABI23374/c  
 ID ABI23374 standard; DNA; 12 BP.  
 XX AC  
 XX ABI23374;  
 XX  
 XX 22-FEB-2002 (first entry)  
 DT  
 DE Oligonucleotide primer SEQ ID NO 323347 for detecting SNP TSC0031342.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 PN  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 PR  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PT  
 PS Claim 1; SEQ ID NO 323347; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;  
 Query Match 27.9%; Score 7.8; DB 1; Length 12;  
 Best Local Similarity 81.8%; Pred. No. 3.4e+02;  
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 5 CCTACGGTGA 15  
 DB 11 CCTACACGTA 1  
 RESULT 596  
 ABI18399/c  
 ID ABI18399 standard; DNA; 12 BP.  
 XX AC  
 XX ABI18399;  
 XX  
 XX 22-FEB-2002 (first entry)  
 DT  
 DE Oligonucleotide primer SEQ ID NO 318372 for detecting SNP TSC0028620.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 PN WO200177384-A2.  
 XX  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 PR  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PT  
 PS Claim 1; SEQ ID NO 318372; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 27.9%; Score 7.8; DB 1; Length 12;  
 Best Local Similarity 81.8%; Pred. No. 3.4e+02;  
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 12 TGTACAGGAG 22  
 DB 12 TGTACAGTAG 2  
 RESULT 597  
 ABF18031/c  
 ID ABF18031 standard; DNA; 13 BP.  
 XX AC  
 XX ABF18031;  
 XX  
 XX 21-FEB-2002 (first entry)  
 DT  
 DE Oligonucleotide SEQ ID NO 118028 for detecting SNP TSC0029509.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 PN WO200177384-A2.  
 XX  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 PR



PA (EPiG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 118028; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 27.9%; Score 7.8; DB 1; Length 13;  
Best Local Similarity 81.8%; Pred. No. 3.8e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 12 TGTACAGGGAG 22  
DB 13 TGTAGAGGTAG 3  
RESULT 598  
ABF18030  
ID ABF18030 standard; DNA; 13 BP.  
XX  
XX ABF18030;  
XX 21-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 118027 for detecting SNP TSC0029509.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPiG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 118027; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 27.9%; Score 7.8; DB 1; Length 13;  
Best Local Similarity 81.8%; Pred. No. 3.8e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 12 TGTACAGGGAG 22  
DB 1 TGTAGAGGTAG 11  
RESULT 599  
ABF19283/C  
ID ABF19283 standard; DNA; 13 BP.  
XX  
XX ABF19283;  
XX 21-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 119280 for detecting SNP TSC0029787.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPiG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 119280; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 4 A; 3 C; 1 G; 4 T; 0 U; 1 Other;  
SQ

```
Query Match      27.9%; Score 7.8; DB 1; Length 13;
Best Local Similarity 69.2%; Pred. No. 3.8e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 TGTACAGGGAGTC 24
      ||||| |||||
Db      13 TGTAAACGTAGTY 1

RESULT 600
ABF4695/c
ID ABF44695 standard; DNA; 13 BP.
XX
AC ABF44695;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 144692 for detecting SNP TSC0036396.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 144692; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 1 Other;
XX
Query Match      27.9%; Score 7.8; DB 1; Length 13;
Best Local Similarity 69.2%; Pred. No. 3.8e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 TGTACAGGGAGTC 24
      ||||| |||||
Db      13 TGTAGACGTAGTY 1

RESULT 601
ABF19282
ID ABF19282 standard; DNA; 13 BP.
```

```
XX ABF19282;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 119279 for detecting SNP TSC0029787.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 119279; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 1 C; 3 G; 4 T; 0 U; 1 Other;
XX
Query Match      27.9%; Score 7.8; DB 1; Length 13;
Best Local Similarity 69.2%; Pred. No. 3.8e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 TGTACAGGGAGTC 24
      ||||| |||||
Db      1 TGTAAACGTAGTY 13

RESULT 602
ABF4694
ID ABF44694 standard; DNA; 13 BP.
XX
AC ABF44694;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 144691 for detecting SNP TSC0036396.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
```



CC oligomers are also used for detecting cell type differentiation. ABC000010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI92073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 3 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 27.9%; Score 7.8; DB 1; Length 13;  
 Best Local Similarity 81.8%; Pred. No. 3.8e+02;  
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTACGGTGATCA 17  
 |||||  
 Db 3 CTCCTGTATCA 13

RESULT 605  
 ADB01855/c  
 ID ADB01855 standard; DNA; 25 BP.

XX ADB01855;  
 AC ADB01855;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human MDZ3 scanning oligonucleotide SEQ ID 2841.  
 XX  
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.

XX Homo sapiens.

OS  
 XX  
 PN EP1281758-A2.  
 XX  
 PD 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MDZ3,  
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 2841; 103pp; English.

XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder,  
 CC associated with decreased or increased expression or activity of MDZ3,  
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 25 BP; 3 A; 7 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 27.9%; Score 7.8; DB 1; Length 25;  
 Best Local Similarity 63.2%; Pred. No. 5.3e+02;  
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 GCCCTACGTGTACAGGGAG 22  
 |||||  
 Db 23 GCACTCGCTGCACACGTAG 5

RESULT 606  
 ADB01856/c  
 ID ADB01856 standard; DNA; 25 BP.

XX ADB01856;  
 AC ADB01856;  
 XX

DT 20-NOV-2003 (first entry)

XX Human MDZ3 scanning oligonucleotide SEQ ID 2842.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.

XX Homo sapiens.

XX EP1281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MDZ3,  
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 2842; 103pp; English.

XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder,  
 CC associated with decreased or increased expression or activity of MDZ3,  
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 25 BP; 3 A; 7 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 27.9%; Score 7.8; DB 1; Length 25;  
 Best Local Similarity 63.2%; Pred. No. 5.3e+02;  
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 GCCCTACGTGTACAGGGAG 22  
 |||||  
 Db 22 GCACTCGCTGCACACGTAG 4

```

RESULT 607
ADB01854/c
ID   ADB01854 standard; DNA; 25 BP.
XX
XX
AC   ADB01854;
XX
XX   20-NOV-2003 (first entry)
DT
XX
XX   Human MDZ3 scanning oligonucleotide SEQ ID 2840.
DE
XX
XX   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
XX   Homo sapiens.
OS
XX
XX   EP1281758-A2.
FN
XX
XX   05-FEB-2003.
PD
XX
XX   30-JUL-2002; 2002EP-00016874.
PF
XX
XX   02-AUG-2001; 2001US-00922181.
PR
XX
XX   (AEOM-) AEOMICA INC.
PA
XX
XX   Shannon M, Gu Y, Nguyen C;
PI
XX
XX   WPI; 2003-423107/40.
DR
XX
XX   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MD24, MD27 or MD212, e.g. cancer.
XX
XX   Example 8; SEQ ID NO 2840; 103pp; English.
PS
XX
XX   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MD24, MD27, MD212. MDZ3 is
CC   encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC   MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC   15q26.1. The MDZ3, MD24, MD27, and MD212 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MD24, MD27, or MD212. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MD24, MD27, or MD212 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
XX   Sequence 25 BP; 4 A; 7 C; 9 G; 5 T; 0 U; 0 Other;
SQ
XX
XX   Query Match      27.9%; Score 7.8; DB 1; Length 25;
XX   Best Local Similarity 63.2%; Pred. No. 5.3e+02;
XX   Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY   4   GCCCTACGTTACAGGGAG 22
    ||| ||| ||| |||
DB   24   GCACCTCGCTGCACACGTAG 6

RESULT 608
ADB01853/c
ID   ADB01853 standard; DNA; 25 BP.
XX
XX
AC   ADB01853;
XX
XX   20-NOV-2003 (first entry)
DT
XX
XX   Human MDZ3 scanning oligonucleotide SEQ ID 2843.
DE
XX
XX   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
XX   Homo sapiens.
OS
XX
XX   EP1281758-A2.
FN
XX
XX   05-FEB-2003.
PD
XX
XX   30-JUL-2002; 2002EP-00016874.
PF
XX
XX   02-AUG-2001; 2001US-00922181.
PR
XX
XX   (AEOM-) AEOMICA INC.
PA
XX
XX   Shannon M, Gu Y, Nguyen C;
PI
XX
XX   WPI; 2003-423107/40.
DR
XX
XX   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MD24, MD27 or MD212, e.g. cancer.
XX
XX   Example 8; SEQ ID NO 2840; 103pp; English.
PS
XX
XX   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MD24, MD27, MD212. MDZ3 is
CC   encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC   MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC   15q26.1. The MDZ3, MD24, MD27, and MD212 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MD24, MD27, or MD212. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MD24, MD27, or MD212 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
XX   Sequence 25 BP; 4 A; 7 C; 9 G; 5 T; 0 U; 0 Other;
SQ
XX
XX   Query Match      27.9%; Score 7.8; DB 1; Length 25;
XX   Best Local Similarity 63.2%; Pred. No. 5.3e+02;
XX   Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY   4   GCCCTACGTTACAGGGAG 22
    ||| ||| ||| |||
DB   24   GCACCTCGCTGCACACGTAG 6

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DT
XX
XX   20-NOV-2003 (first entry)
DE
XX
XX   Human MDZ3 scanning oligonucleotide SEQ ID 2839.
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
XX   Homo sapiens.
OS
XX
XX   EP1281758-A2.
FN
XX
XX   05-FEB-2003.
PD
XX
XX   30-JUL-2002; 2002EP-00016874.
PF
XX
XX   02-AUG-2001; 2001US-00922181.
PR
XX
XX   (AEOM-) AEOMICA INC.
PA
XX
XX   Shannon M, Gu Y, Nguyen C;
PI
XX
XX   WPI; 2003-423107/40.
DR
XX
XX   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MD24, MD27 or MD212, e.g. cancer.
XX
XX   Example 8; SEQ ID NO 2839; 103pp; English.
PS
XX
XX   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MD24, MD27, MD212. MDZ3 is
CC   encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC   MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC   15q26.1. The MDZ3, MD24, MD27, and MD212 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MD24, MD27, or MD212. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MD24, MD27, or MD212 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
XX   Sequence 25 BP; 4 A; 7 C; 10 G; 4 T; 0 U; 0 Other;
SQ
XX
XX   Query Match      27.9%; Score 7.8; DB 1; Length 25;
XX   Best Local Similarity 63.2%; Pred. No. 5.3e+02;
XX   Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY   4   GCCCTACGTTACAGGGAG 22
    ||| ||| ||| |||
DB   25   GCACCTCGCTGCACACGTAG 7

RESULT 609
ADB01857/c
ID   ADB01857 standard; DNA; 25 BP.
XX
XX
AC   ADB01857;
XX
XX   20-NOV-2003 (first entry)
DT
XX
XX   Human MDZ3 scanning oligonucleotide SEQ ID 2843.
DE
XX
XX   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX

```

XX OS Homo sapiens.  
 XX PN EP1281758-A2.  
 XX PD 05-FEB-2003.  
 XX PF 30-JUL-2002; 2002EP-00016874.  
 XX PR 02-AUG-2001; 2001US-00922181.  
 XX PA (AEOM-) AEOMICA INC.  
 XX PI Shannon M, Gu Y, Nguyen C;  
 XX WI 2003-423107/40.  
 XX PT New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 XX Example 8; SEQ ID NO 2843; 103pp; English.  
 XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX Sequence 25 BP; 4 A; 7 C; 9 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 27.9%; Score 7.8; DB 1; Length 25;  
 Best Local Similarity 63.2%; Pred. No. 5.3e+02;  
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 4 GCCTACGTTACAGGGAG 22  
 DB |||||  
 21 GCCTCGCTGCACACGTAG 3  
 RESULT 610  
 ADB01858/c  
 ID ADB01858 standard; DNA; 25 BP.  
 AC ADB01858;  
 XX 20-NOV-2003 (first entry)  
 DT Human MD23 scanning oligonucleotide SEQ ID 2844.  
 DE Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX Homo sapiens.  
 OS EP1281758-A2.  
 XX 05-FEB-2003.  
 XX 30-JUL-2002; 2002EP-00016874.  
 XX PF

XX PR 02-AUG-2001; 2001US-00922181.  
 XX PA (AEOM-) AEOMICA INC.  
 XX PI Shannon M, Gu Y, Nguyen C;  
 XX WI 2003-423107/40.  
 XX PT New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 XX Example 8; SEQ ID NO 2844; 103pp; English.  
 XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX Sequence 25 BP; 5 A; 6 C; 9 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 27.9%; Score 7.8; DB 1; Length 25;  
 Best Local Similarity 63.2%; Pred. No. 5.3e+02;  
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 4 GCCTACGTTACAGGGAG 22  
 DB |||||  
 20 GCCTCGCTGCACACGTAG 2  
 RESULT 611  
 AAF47954  
 ID AAF47954 standard; DNA; 15 BP.  
 AC AAF47954;  
 XX 30-MAR-2001 (first entry)  
 DT IGFBP3 oligonucleotide #1374.  
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth factor 1 receptor; IGF-1; ptyriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX Homo sapiens.  
 OS WO200078341-A1.  
 XX 28-DEC-2000.  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX 21-JUN-1999; 99US-0140345P.  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 PA

XX Wright CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisenescence nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX Example 7; Page 53; 201pp; English.  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisenescence oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisenescence  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX Sequence 15 BP; 3 A; 8 C; 2 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 27.1%; Score 7.6; DB 1; Length 15;  
 Best Local Similarity 71.4%; Pred. No. 4.8e+02;  
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 5 CCTACGGTGACAG 18  
 Db 2 CACTCCCGGTACAG 15  
 RESULT 612  
 AAF47955  
 ID AAF47955 standard; DNA; 15 BP.  
 AC AAF47955;  
 XX 30-MAR-2001 (first entry)  
 DT IGFBP3 oligonucleotide #1375.  
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 XX cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX Homo sapiens.  
 OS WO200078341-A1.  
 PN 28-DEC-2000.  
 XX 21-JUN-2000; 2000WO-AU000693.  
 PF 21-JUN-1999; 99US-0140345P.  
 PR (MURD-) MURDOCH CHILDRENS RES INST.  
 XX Wright CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisenescence nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX Example 7; Page 53; 201pp; English.  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisenescence oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisenescence  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX Sequence 15 BP; 3 A; 7 C; 2 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 27.1%; Score 7.6; DB 1; Length 15;  
 Best Local Similarity 71.4%; Pred. No. 4.8e+02;  
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 5 CCTACGGTGACAG 18  
 Db 1 CACTCCCGGTACAG 14  
 RESULT 613  
 AAF47956  
 ID AAF47956 standard; DNA; 15 BP.  
 AC AAF47956;  
 XX 30-MAR-2001 (first entry)  
 DT IGFBP3 oligonucleotide #1376.  
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 XX cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX Homo sapiens.  
 OS WO200078341-A1.  
 PN 28-DEC-2000.  
 XX 21-JUN-2000; 2000WO-AU000693.  
 PF 21-JUN-1999; 99US-0140345P.  
 PR (MURD-) MURDOCH CHILDRENS RES INST.  
 XX Wright CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisenescence nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.  
 XX  
 PS Example 7; Page 53; 201pp; English.  
 XX  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for insulin-like growth factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAP45151 and AAP45153-  
 CC P45361). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, seborrheas, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 27.1%; Score 7.6; DB 1; Length 15;  
 Best Local Similarity 71.4%; Pred. No. 4.8e+02;  
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 7 CTACGCTACAGG 20  
 Db 2 CTCCTCGTACAGTG 15  
 RESULT 614  
 ABA80105/c  
 ID ABA80105 standard; DNA; 17 BP.  
 XX  
 AC ABA80105;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE HBA2 mutation correcting oligonucleotide SEQ ID NO: 2951.  
 XX  
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;  
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;  
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;  
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;  
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;  
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;  
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;  
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;  
 KW Alzheimer's disease; cytosolic; antiskilling; antiandemic; haemostatic;  
 KW antileptic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200173002-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 27-MAR-2001; 2001WO-US009761.  
 XX  
 PR 27-MAR-2000; 2000US-0192176P.  
 PR 27-MAR-2000; 2000US-0192179P.  
 PR 01-JUN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 XX  
 XX (UYDE ) UNIV DELAWARE.  
 PA  
 XX Kmiec EB, Gamper HB, Rice MC;  
 XX WPI; 2001-639230/73.  
 DR  
 XX Oligonucleotide for targeted alterations of genetic sequences and for  
 PT treating cystic fibrosis, comprises at least one mismatch and chemical

PT modification.  
 XX  
 PS Claim 7; Page 208; 294pp; English.  
 XX  
 CC The present invention provides single-stranded oligonucleotides which can  
 CC be used for the targeted alteration of genomic sequences, where the  
 CC oligonucleotide has at least one mismatch compared with the genomic  
 CC sequence to be altered. In particular, these sequences are directed at  
 CC the following genes: adenosine deaminase, p53, beta-globin,  
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A  
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus  
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,  
 CC apolipoprotein E (APOE), LDL receptor (LDLR), presenilin-1 (PSEN1) and  
 CC (UGT1), amyloid precursor protein (APP), presenilin-1 (PSEN1) and  
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases  
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,  
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,  
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and  
 CC various syndromes. The present sequence is one of the gene correcting  
 CC oligonucleotides of the invention  
 XX  
 SQ Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
 Query Match 27.1%; Score 7.6; DB 1; Length 17;  
 Best Local Similarity 71.4%; Pred. No. 5.2e+02;  
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 6 CCTACGCTACAGG 19  
 Db 15 CCTCCCTGACAAAG 2  
 RESULT 615  
 ABA80104  
 ID ABA80104 standard; DNA; 17 BP.  
 XX  
 AC ABA80104;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE HBA2 mutation correcting oligonucleotide SRQ ID NO: 2950.  
 XX  
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;  
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;  
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;  
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;  
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;  
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;  
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;  
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;  
 KW Alzheimer's disease; cytosolic; antiskilling; antiandemic; haemostatic;  
 KW antileptic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200173002-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 27-MAR-2001; 2001WO-US009761.  
 XX  
 PR 27-MAR-2000; 2000US-0192176P.  
 PR 27-MAR-2000; 2000US-0192179P.  
 PR 01-JUN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 XX  
 XX (UYDE ) UNIV DELAWARE.  
 PA  
 XX Kmiec EB, Gamper HB, Rice MC;  
 XX WPI; 2001-639230/73.  
 DR  
 XX Oligonucleotide for targeted alterations of genetic sequences and for



PT treating cystic fibrosis, comprises at least one mismatch and chemical  
PT modification.  
XX  
XX Claim 7; Page 208; 294pp; English.  
XX  
XX The present invention provides single-stranded oligonucleotides which can  
XX be used for the targeted alteration of genomic sequences, where the  
XX oligonucleotide has at least one mismatch compared with the genomic  
XX sequence to be altered. In particular, these sequences are directed at  
XX the following genes: adenosine deaminase, p53, beta-globin,  
XX retinoblastoma, BRCA1, BRCA2, CPTA, cyclin-dependent kinase inhibitor 2A  
XX (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus  
XX 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,  
XX apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase  
XX (UGT1), amyloid precursor protein (APP), presenilin-1 (PSEN1) and  
XX presenilin-2 (PSEN2). These can be used in the gene therapy of diseases  
XX such as cancer, adenosine deaminase deficiency, cystic fibrosis,  
XX haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,  
XX Alzheimer's disease, melanoma, adenomatous polyposis of the colon and  
XX various syndromes. The present sequence is one of the gene correcting  
XX oligonucleotides of the invention.  
XX  
XX Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 27.1%; Score 7.6; DB 1; Length 17;  
Best Local Similarity 71.4%; Pred. No. 5.2e+02;  
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 6 CCTACGCTACAGG 19  
Db 3 CTTCCCTGGACAG 16  
RESULT 616  
ADD71263  
ID ADD71263 standard; DNA; 10 BP.  
XX  
XX ADD71263;  
XX  
XX 15-JAN-2004 (first entry)  
XX  
XX Mouse ET gene 5' splice donor site from intron 4.  
XX  
XX Mouse; ethenolaminephosphate cytidyl transferase; ET; ds;  
XX splice donor site; antilipemic; cardiant; anorectic;  
XX phosphatidylethanolamine; Zellweger's syndrome; lipid-related disease;  
XX cardiovascular disease; atherosclerosis; obesity.  
XX  
XX Mus musculus.  
XX  
XX US2003194795-A1.  
XX  
XX 16-OCT-2003.  
XX  
XX 21-MAR-2002; 2002US-00101957.  
XX  
XX 21-MAR-2002; 2002US-00101957.  
XX  
XX (BAKO/) BAKOVIC M.  
XX (POLO/) POLOMIENKO A.  
XX  
XX Bakovic M; Poloumienko A;  
XX  
XX WPI; 2003-844457/78.  
XX  
XX New gene encoding a protein having ethanolaminephosphate  
XX cytidyltransferase activity, useful for treating Zellweger's syndrome, or  
XX lipid-related diseases such as cardiovascular diseases and obesity.  
XX  
XX Example 1; Page 6; 22pp; English.  
XX  
XX The invention relates to a mouse gene encoding a protein having  
XX ethanolaminephosphate cytidyltransferase (ET) activity appearing as

CC ADD71226, a degenerate variant of the ET gene, or a sequence that  
CC hybridises to the complement of the ET gene under stringent conditions.  
CC Also included is a promoter of a human ethanolaminephosphate  
CC cytidyltransferase gene appearing as ADD71227. The gene and promoter are  
CC useful for producing a transgenic animal, and for identifying,  
CC preventing, and treating diseases (by gene therapy) related to  
CC inappropriate phosphatidylethanolamine production, e.g. Zellweger's  
CC syndrome, or lipid-related diseases such as cardiovascular diseases,  
CC atherosclerosis and obesity. The present sequence is a mouse ET gene 5'  
XX splice donor site.  
XX  
XX Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;  
SQ  
Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 3.3e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 14 TACAGGGAG 22  
Db 1 TACAGGTAG 9  
RESULT 617  
AAZ83886/c  
ID AAZ83886 standard; DNA; 10 BP.  
XX  
XX AAZ83886;  
XX  
XX 07-APR-2000 (first entry)  
XX  
XX Metastatic breast tumour cell upregulated transcript tag #3120.  
XX  
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
XX non-metastatic breast tumour tissue; gene therapy; anticancer;  
XX antimetastatic; vaccine; diagnosis; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO965928-A2.  
XX  
XX 23-DEC-1999.  
XX  
XX 18-JUN-1999; 99WO-US013647.  
XX  
XX 19-JUN-1998; 98US-009853P.  
XX 19-JUN-1998; 98US-009897P.  
XX 19-JUN-1998; 98US-0090035P.  
XX 19-JUN-1998; 98US-0090040P.  
XX 19-JUN-1998; 98US-0090041P.  
XX  
XX (GENZ ) GENZYME CORP.  
XX (ROBE/) ROBERTS B L.  
XX (SHAN/) SHANKARA S.  
XX  
XX Roberts BL, Shankara S;  
XX  
XX WPI; 2000-106079/09.  
XX  
XX Isolated polynucleotides differentially expressed between metastatic and  
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and  
XX treatment of cancer.  
XX  
XX Claim 1; Page 142; 219pp; English.  
XX  
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
XX that are preferentially transcribed in the metastatic breast tumour  
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
XX to AAZ86677 represent tags corresponding to distinct transcripts that are  
XX preferentially transcribed in the primary or non-metastatic breast tumour  
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These  
XX transcripts can be used for diagnosis, prognosis, monitoring and  
XX treatment of breast cancer, particularly where metastatic. Diagnosis is  
XX by standard immunoassays or hybridisation/amplification reactions.

CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 CC  
 CC Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 3.3e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 AGCTGTACA 17  
 |||||  
 Db 10 ACCTGTACA 2

## RESULT 618

AAF37857  
 ID AAF37857 standard; DNA; 10 BP.

XX AAF37857;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4596.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UJJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags; useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 164; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX

SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 26.4%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 3.3e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGG 19

|||||  
 Db 2 GTGTACAGG 10

## RESULT 619

ABH73586

ID ABH73586 standard; DNA; 12 BP.

XX ABH73586;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 273571 for detecting SNP TSC0003234.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 273571; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 26.4%; Score 7.4; DB 1; Length 12;  
 Best Local Similarity 88.9%; Pred. No. 4.1e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGCTGATC 16  
 |||||  
 Db 3 TACGCTGATC 11

RESULT 620

AAQ87648  
 ID AAQ87648 standard; DNA; 18 BP.

XX

XX

AC AAQ87648;

XX

DT 19-DEC-1995 (first entry)

XX

DE Chick antisense oligonucleotide to p75 NGFR gene.

XX

KW Oligonucleotide; antisense; down-regulation; expression; trauma;

KW nerve growth factor receptor; neurodegenerative disease; Alzheimer's;

KW Parkinson's; Huntington's disease; multiple sclerosis;

KW vascular ischaemia; stroke; ss.

XX

OS Synthetic.

XX

XX WO9511253-A1.

PN

XX

PD 27-APR-1995.

XX

XX 18-OCT-1994; 94WO-AU000631.

PF

XX

PR 18-OCT-1993; 93AU-00001870.

XX

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PA

XX

PI Barrett GL;

XX

XX WPI; 1995-170186/22.

DR

XX

XX Anti-sense oligo:nucleotide(s) to nerve growth factor receptor gene - of

PT p75 NGFR, down-regulate expression and enhance neurone survival; for

PT treating cerebral palsy, Alzheimer's disease, stroke, etc.

XX

XX Example 3; Page 35; 59pp; English.

XX

CC The sequence of an antisense oligonucleotide to the chick nerve growth

CC factor receptor (NGFR) gene which was used as a control for the survival

CC of mouse dorsal root ganglial (DRG) cells treated with oligonucleotides

CC AAQ87641-2. These oligonucleotides are antisense sequences directed at

CC down-regulating the expression of the gene encoding the mouse p75 NGFR

CC gene. The oligonucleotides can be used in methods to treat

CC neurodegenerative conditions associated with disease and/or trauma such

CC as Alzheimer's, Parkinson's or Huntington's disease, multiple sclerosis,

CC vascular ischaemia associated with stroke, etc

XX

SQ Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

XX

Query Match 26.4%; Score 7.4; DB 1; Length 18;

Best Local Similarity 54.7%; Pred. No. 5.8e+02;

Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 11 GTGCTACAGGAGTCCAG 27

XX

Db 2 GTGCTACGCTGTCAG 18

XX

RESULT 621

ABI23376

ID ABI23376 standard; DNA; 12 BP.

XX

AC ABI23376;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 323349 for detecting SNP TSC0031342.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

XX (EPIG-) EPIGENOMICS AG.

PA

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

XX WPI; 2001-657177/75.

DR

XX

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX

XX Claim 1; SEQ ID NO 323349; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -AB09989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

XX

Query Match 25.7%; Score 7.2; DB 1; Length 12;

Best Local Similarity 75.0%; Pred. No. 4.6e+02;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 TACGCTGATCAGG 19

XX

Db 1 TACGCTGATGAGG 12

XX

RESULT 622

ABH73584/c

ID ABH73584 standard; DNA; 12 BP.

XX

AC ABH73584;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 273569 for detecting SNP TSC0003234.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

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OS Homo sapiens.
XX
XX PN WC200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG..
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 273569; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 25.7%; Score 7.2; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 4.6e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CCTACGTGTACA 17
DB 12 CGTACACGTACA 1

RESULT 623
AAZ41746
ID AAZ41746 standard; DNA; 12 BP.
XX
XX AC AAZ41746;
XX
XX DT 20-MAR-2003 (revised)
XX
XX DT 21-JAN-2000 (first entry)
XX
XX DE Organic material detecting primer 107.
XX
XX KW Amplification; polymerase chain reaction; PCR; microorganism; compost;
XX detection; pollutant; soil; food; agricultural chemical; polymer;
XX organochlorine; primer; ss.
XX
XX OS Synthetic.
XX
XX PN DE19914461-A1.
XX
XX PD 21-OCT-1999.
XX
XX PF 30-MAR-1999; 99DE-01014461.
XX
XX PR 31-MAR-1998; 98JP-00087651.
XX
XX PR 16-MAR-1999; 99JP-00069694.
XX
XX PA (SAOL) SANYO ELECTRIC CO LTD.

(NORQ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
XX
XX PI Inoue T;
XX
XX DR WPI; 1999-592157/51.
XX
XX PT Novel polymerase chain reaction method, for differentiating between
XX microorganisms and for detecting contaminants.
XX
XX PS Example 1; Page 19; 78pp; German.
XX
XX CC This invention describes a novel method for the amplification of DNA
XX comprising (i) preparing many primers (P) with different probabilities of
XX amplification and (ii) simultaneous polymerase chain reaction (PCR) of
XX many different DNA using these primers. The method is used (i) to
XX differentiate between different microorganisms in a mixed population and
XX (ii) to determine presence/absence of an impurity (pollutant), or its
XX concentration, in e.g. soil, foods, compost etc., typically metals,
XX agricultural chemicals, polymers, organochlorine compounds etc. A
XX particular use is monitoring composting of organic material.
XX Amplification with many primers produces a lot of information, so
XX reliability of the test is improved, and many samples may be tested
XX quickly. AAZ41640-241855 represent the primers described in the method of
XX the invention. (Updated on 20-MAR-2003 to correct PR field.)
XX
XX SQ Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 25.7%; Score 7.2; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 4.6e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 GTGTACAGGGAG 22
DB 1 GAGTACAGGAG 12

RESULT 624
AAZ41530
ID AAZ41530 standard; DNA; 12 BP.
XX
XX AC AAZ41530;
XX
XX DT 19-JAN-2000 (first entry)
XX
XX DE Microbe detection in organic waste arbitrarily primed PCR primer #107.
XX
XX KW Microbe; detection; organic waste; arbitrarily primer PCR;
XX random amplified polymorphic DNA; amplification; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX PN JF11276176-A.
XX
XX PD 12-OCT-1999.
XX
XX PF 31-MAR-1998; 98JP-00087652.
XX
XX PR 31-MAR-1998; 98JP-00087652.
XX
XX PA (SAOL) SANYO ELECTRIC CO LTD.
XX
XX PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
XX DR WPI; 1999-626940/54.
XX
XX PT Amplification of a DNA fragment - in order to establish the state of
XX existence of a microbe.
XX
XX PS Claim 1; Page 9; 40pp; Japanese.
XX
XX CC A method has been developed for the amplification of a DNA fragment in
XX which amplification is carried out on the DNA fragments of a number of
XX different DNAs. The method comprises a PCR reaction repeatedly carrying
XX out a heat-denaturing step, a primer annealing step and a polymerase

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CC extending step, to amplify the DNA fragments of a plural of different  
 CC DNAs. The method can detect the existence of a microbe in organic waste.  
 CC AA241424 to AA241639 represent PCR primers used in random amplified  
 CC polymorphic DNA arbitrarily primed PCR, for the detection of microbes in  
 CC organic waste  
 XX  
 XX Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 25.7%; Score 7.2; DB 1; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 4.6e+02;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 11 GTGTACAGGGAG 22  
 Db 1 GAGTACACGAAG 12  
 RESULT 625  
 AAC97881  
 ID AAC97881 standard; DNA; 12 BP.  
 XX  
 AC AAC97881;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 DE Primer used to illustrate DNA amplification method SEQ ID 107.  
 DE  
 XX Primer; amplification; selective; ss.  
 KW  
 XX  
 OS Synthetic.  
 XX  
 XX JP2000270867-A.  
 PN  
 XX  
 XX 03-OCT-2000.  
 PD  
 XX  
 PF 19-MAR-1999; 99JP-00076844.  
 XX  
 PR 19-MAR-1999; 99JP-00076844.  
 XX  
 PA (SAOL) SANYO ELECTRIC CO LTD.  
 PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.  
 XX  
 DR WPI; 2001-011047/02.  
 XX  
 XX Amplification of a DNA fragment and its apparatus.  
 FT  
 XX  
 PS Example 1; Page 9; 32pp; Japanese.  
 XX  
 CC This invention relates to a method for amplifying a DNA fragment. The  
 CC method comprises successive repetitions of heat-denaturing, annealing of  
 CC a primer and an extending step using a DNA polymerase. The method makes  
 CC use of a cDNA pool in which the primer is one primer or a pair of primer  
 CC sets and has an amplification probability which allows it to amplify a  
 CC DNA fragment from a limited number of the cDNAs among the DNA pool (where  
 CC the limited number is in the range of 1 to 25). Also included in the  
 CC invention are apparatus used for carrying out the method, a primer and a  
 CC DNA polymerase and a kit used for amplifying a DNA fragment. The method  
 CC can be used to amplify a limited number of cDNAs from a pool in which a  
 CC wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990  
 CC represent primers used in an example illustrating the method of the  
 CC invention  
 XX  
 SQ Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
 Query Match 25.7%; Score 7.2; DB 1; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 4.6e+02;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 11 GTGTACAGGGAG 22  
 Db 1 GAGTACACGAAG 12

RESULT 626  
 ABH73580/c  
 ID ABH73580 standard; DNA; 12 BP.  
 XX  
 AC ABH73580;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 273565 for detecting SNP TSC0003234.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 273565; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;  
 Query Match 25.7%; Score 7.2; DB 1; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 4.6e+02;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 6 CCTACGCTGACA 17  
 Db 12 CATACACGTACA 1  
 RESULT 627  
 ABH30582/c  
 ID ABH30582 standard; DNA; 13 BP.  
 XX  
 AC ABH30582;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 230559 for detecting SNP TSC0056234.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX

XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB0000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 230559; 29pp + Sequence Listing; German.  
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX SQ Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 25.7%; Score 7.2; DB 1; Length 13;  
Best Local Similarity 75.0%; Pred. No. 5e+02;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 10 CGGTGACAGGA 21  
Db 13 CGTATACAGTA 2  
RESULT 628  
ABC62971  
ID ABC62971 standard; DNA; 13 BP.  
AC ABC62971;  
XX 21-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 62988 for detecting SNP TSC0016657.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX OS  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB0000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 62987; 29pp + Sequence Listing; German.  
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX SQ Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 25.7%; Score 7.2; DB 1; Length 13;  
Best Local Similarity 75.0%; Pred. No. 5e+02;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 10 CGGTGACAGGA 21  
Db 13 CGTATACAGTA 2  
RESULT 628  
ABC62971  
ID ABC62971 standard; DNA; 13 BP.  
AC ABC62971;  
XX 21-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 62988 for detecting SNP TSC0016657.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX OS  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB0000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 62987; 29pp + Sequence Listing; German.  
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX SQ Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 25.7%; Score 7.2; DB 1; Length 13;  
Best Local Similarity 75.0%; Pred. No. 5e+02;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 10 CGGTGACAGGA 21  
Db 13 CGTATACAGTA 2  
RESULT 628  
ABC62971  
ID ABC62971 standard; DNA; 13 BP.  
AC ABC62971;  
XX 21-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 62987 for detecting SNP TSC0016657.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX OS  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB0000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 62987; 29pp + Sequence Listing; German.  
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX SQ Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 25.7%; Score 7.2; DB 1; Length 13;  
Best Local Similarity 75.0%; Pred. No. 5e+02;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 8 TACGTGTACAG 19  
Db 2 TACCTTTACAG 13

PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX Claim 1; SEQ ID NO 62988; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
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XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX SQ Sequence 13 BP; 3 A; 4 C; 1 G; 5 T; 0 U; 0 Other;  
Query Match 25.7%; Score 7.2; DB 1; Length 13;  
Best Local Similarity 75.0%; Pred. No. 5e+02;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 8 TACGTGTACAG 19  
Db 2 TACCTTTACAG 13  
RESULT 629  
ABC62970/C  
ID ABC62970 standard; DNA; 13 BP.  
XX AC ABC62970;  
XX 21-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 62987 for detecting SNP TSC0016657.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX OS  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB0000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX Claim 1; SEQ ID NO 62987; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX SQ Sequence 13 BP; 3 A; 4 C; 1 G; 5 T; 0 U; 0 Other;  
Query Match 25.7%; Score 7.2; DB 1; Length 13;  
Best Local Similarity 75.0%; Pred. No. 5e+02;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 8 TACGTGTACAG 19  
Db 2 TACCTTTACAG 13

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 5 A; 1 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 25.7%; Score 7.2; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 5e+02;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 8 TACGTTACAGG 19  
 Db 12 TACCTTACAG 1  
 RESULT 630  
 ABC62969  
 ID ABC62969 standard; DNA; 13 BP.  
 XX AC ABC62969;  
 XX DT 21-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 62986 for detecting SNP TSC0016657.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 PI Olek A, Piepenbrock C, Berlin K;  
 DR WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 62986; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 25.7%; Score 7.2; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 5e+02;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 8 TACGTTACAGG 19  
 Db 12 TACCTTACAG 1  
 RESULT 632  
 ABH30583  
 ID ABH30583 standard; DNA; 13 BP.  
 XX AC ABH30583;  
 XX DT 21-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 62985 for detecting SNP TSC0016657.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 PI Olek A, Piepenbrock C, Berlin K;  
 DR WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 62985; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 25.7%; Score 7.2; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 5e+02;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 8 TACGTTACAGG 19  
 Db 12 TACCTTACAG 1

Best Local Similarity 75.0%; Pred. No. 5e+02;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 8 TACGTTACAGG 19  
 Db 2 TACCTTACAG 13  
 RESULT 631  
 ABC62968/c  
 ID ABC62968 standard; DNA; 13 BP.  
 XX AC ABC62968;  
 XX DT 21-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 62995 for detecting SNP TSC0016657.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 PI Olek A, Piepenbrock C, Berlin K;  
 DR WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 62985; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;  
 Query Match 25.7%; Score 7.2; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 5e+02;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 8 TACGTTACAGG 19  
 Db 12 TACCTTACAG 1  
 RESULT 632  
 ABH30583  
 ID ABH30583 standard; DNA; 13 BP.  
 XX AC ABH30583;  
 XX DT 21-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 62995 for detecting SNP TSC0016657.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 PI Olek A, Piepenbrock C, Berlin K;  
 DR WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 62985; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;  
 Query Match 25.7%; Score 7.2; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 5e+02;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 8 TACGTTACAGG 19  
 Db 12 TACCTTACAG 1

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XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 230560 for detecting SNP TSC0056234.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX ZN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 230560; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF9989, ABE00010-ABE9989 and AB100010-AB182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the invention. NOTE: The sequence
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 25.7%; Score 7.2; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 CGTGTCACAGGGA 21
    ||| ||| ||| |||
Db 1 CGTATACACGTA 12

RESULT 633
AAA52434
ID AAA52434 standard; DNA; 15 BP.
XX AC AAA52434;
XX DT 18-SEP-2000 (first entry)
XX DE Tdt-expressing Ramos cell VH insertion+deletion mutation, F264.
XX KW Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M;
XX KW IgM; V gene diversity; directed constitutive hypermutation;
XX KW target sequence diversification; terminal deoxynucleotidyl transferase;
XX KW Tdt; clonal expansion; selection; heavy chain variable region; VH;
XX KW mutant; ds.
XX OS Homo sapiens.
XX OS Synthetic.

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XX PN WO200022111-A1.
XX PD 20-APR-2000.
XX PF 08-OCT-1999; 99WO-GB003358.
XX PR 09-OCT-1998; 98GB-00022104.
XX PR 13-JAN-1999; 99GB-00001141.
XX PR 09-JUN-1999; 99GB-00013435.
XX PA (MEDI-) MEDICAL RES COUNCIL.
XX PI Sale JE, Neuberger MS, Cumbers SJ;
XX DR WPI; 2000-317971/27.
XX PT Lymphoid cell line preparation useful for producing gene products having
XX PT desired activity, involves screening and selecting cells having ongoing
XX PT target sequence diversification and higher mutation rates.
XX PS Example 4; Fig 6; 69pp; English.
XX CC The invention relates to a method of preparing a lymphoid cell line
XX CC capable of directed constitutive hypermutation of a target
XX CC nucleic acid region. The method comprises screening a cell population for
XX CC ongoing target sequence diversification and selecting a cell in which the
XX CC rate of target nucleic acid mutation exceeds that of other nucleic acid
XX CC mutation by a factor of 100 or more. The invention also relates to a
XX CC method for preparing a gene product with a desired activity, comprising
XX CC expressing a nucleic acid encoding the target gene operably linked to a
XX CC sequence which directs hypermutation e.g., terminal deoxynucleotidyl
XX CC transferase (Tdt), in the lymphoid cell line, and identifying a cell or
XX CC cells which express a mutated gene product with the desired activity. One
XX CC or more clonal populations of the identified cells is established, and
XX CC cells with an improved activity of interest are selected. These steps may
XX CC be iteratively repeated until a gene product with a desired activity
XX CC is obtained. The cell lines prepared according to the method of the
XX CC invention are used for directed constitutive hypermutation of a nucleic
XX CC acid region in the preparation of a gene product, preferably an enzyme or
XX CC of the invention, IgM-secreting Ramos cells were selected for use as they
XX CC undergo hypermutation during clonal expansion. This was determined on the
XX CC basis of the amount of diversity in the heavy chain variable region (VH).
XX CC Sequences AAA52366-A52434 represent fragments of Ramos cell VH region DNA
XX CC containing mutations other than single nucleotide substitutions. The
XX CC number assigned to the mutation represents the position in the wild-type
XX CC VH DNA (AAA52364) to which the first nucleotide in the mutant fragment
XX CC corresponds. Sequences AAA52388-A52434 represent mutations that occur in
XX CC Ramos cells which express Tdt, and sequences AAA52366-A52487 represent
XX CC mutations that occur in non-Tdt- expressing control Ramos cells
XX SQ Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 25.7%; Score 7.2; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 5.6e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GTGTACAGGGAG 22
    ||| ||| ||| |||
Db 3 GTGCATCGGG 14

RESULT 634
AAZ62686/C
ID AAZ62686 standard; RNA; 15 BP.
XX AC AAZ62686;
XX DT 28-MAR-2000 (first entry)
XX DE Substrate for HH ribozyme HCV-5596 which cleaves HCV RNA at nt. 5596.

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KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;  
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;  
 XX autoimmune disease; ss.  
 OS Hepatitis C virus.  
 XX WO9955847-A2.  
 PN 04-NOV-1999.  
 XX 26-APR-1999; 99WO-US009027.  
 XX 27-APR-1998; 98US-0083217P.  
 PR 18-SEP-1998; 98US-0100842P.  
 PR 25-FEB-1999; 98US-00257608.  
 PR 23-MAR-1999; 99US-00274553.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;  
 PI WPI; 2000-062023/05.  
 DR Novel ribozymes for the treatment of diseases and conditions related to  
 PT hepatitis C infection.  
 PT Claim 1; Page 59; 123pp; English.  
 XX The present sequence represents the preferred target sequence of an  
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in  
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme  
 CC target sites using a computer folding algorithm and regions of the mRNA  
 CC which did not form secondary folding structures and contained potential  
 CC ribozyme cleavage sites were identified. Ribozymes were synthesized to  
 CC target these sites and their activities optimized by either varying the  
 CC length of the binding arms or by modification to prevent degradation by  
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or  
 CC viral replication, and are used to treat diseases associated with  
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and  
 CC hepatocellular carcinoma. The ribozymes may be used in combination with  
 CC interferon to treat HCV infection, other infectious diseases, autoimmune  
 CC diseases, and cancer  
 XX Sequence 15 BP; 2 A; 2 C; 8 G; 0 T; 3 U; 0 Other;  
 SQ Query Match 25.7%; Score 7.2; DB 1; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 5.6e+02;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 15 ACAGGGAGTCCA 26  
 Db |||||  
 13 ACCTGGAGTCCA 2  
 RESULT 635  
 ABX00537/c  
 ID ABX00537 standard; RNA; 15 BP.  
 XX AC ABX00537;  
 XX 23-DEC-2002 (first entry)  
 XX Hepatitis C virus substrate #319 for HCV hammerhead ribozyme #319.  
 DE Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
 XX HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;  
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
 KW type I interferon; interferon alpha; interferon beta; cytostatic;  
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;  
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.  
 XX Hepatitis C virus.  
 OS

XX US2002082225-A1.  
 PN 27-JUN-2002.  
 PD 23-MAR-1999; 99US-00274553.  
 PF 23-MAR-1999; 99US-00274553.  
 PR (BLAT/) BLATT L.  
 XX (MCSW/) MCSWIGGEN J A.  
 PA (ROBE/) ROBERTS B.  
 PA (PAVC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;  
 PI WPI; 2002-617759/66.  
 DR New ribozymes targeting RNA derived from hepatitis C virus inhibit viral  
 XX replication and are useful to treat hepatitis C virus infections and  
 PT cirrhosis, liver failure or hepatocellular carcinoma.  
 PT Claim 1; Page 30; 80pp; English.  
 XX The present invention relates to enzymatic nucleic acids which  
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The  
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin  
 CC (HP) motif where the binding arms comprise sequences complementary to one  
 CC of the substrate sequences defined in the specification. The HCV  
 CC ribozymes are useful for modulating the expression and/or replication of  
 CC HCV. They can be used to treat cirrhosis, liver failure and/or  
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating  
 CC a condition associated with HCV infection in conjunction with one or more  
 CC other drug therapies, particularly type I interferon, especially  
 CC interferon alpha, beta or gamma or consensus interferon. The present  
 CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:  
 CC Some of the sequence data for this patent did not form part of the  
 CC printed specification. The complete sequence data for this patent was  
 CC obtained in electronic format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipsDIDEntry.html  
 XX Sequence 15 BP; 2 A; 2 C; 8 G; 0 T; 3 U; 0 Other;  
 SQ Query Match 25.7%; Score 7.2; DB 1; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 5.6e+02;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 15 ACAGGGAGTCCA 26  
 Db |||||  
 13 ACCTGGAGTCCA 2  
 RESULT 636  
 AAF43233  
 ID AAF43233 standard; DNA; 10 BP.  
 XX AC AAF43233;  
 XX 23-MAR-2001 (first entry)  
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11372.  
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 XX linker; PCR primer; ds.  
 OS Saccharomyces cerevisiae.  
 XX WO2000077214-A2.  
 PN 21-DEC-2000.  
 PD

XX 14-JUN-2000; 2000WO-US016223.  
 XX 16-JUN-1999; 99US-00335032.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 XX gene expression (SAGE) tags, useful for studying, monitoring and  
 XX affecting phases of the cell cycle.  
 XX Example; Page 356; 419pp; English.  
 XX The present invention describes an isolated DNA molecule comprising a  
 XX coding sequence of a yeast gene selected from a group of 745 NORF (not  
 XX previously assigned open reading frame; or nonannotated ORF) genes  
 XX comprising a SAGE (serial analysis of gene expression) tag. Also  
 XX described are: (1) a method (M1) of using NORF genes to affect the cell  
 XX cycle comprising administering a NORF gene whose expression varies by at  
 XX least 10% between any two phases of the cell cycle selected from log  
 XX phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 XX antifungal drugs comprising: (a) contacting a test substance with a yeast  
 XX cell; and (b) monitoring expression of a NORF gene whose expression  
 XX varies as in M1, where a test substance which modifies the expression of  
 XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 XX identifying human genes which are involved in cell cycle progression  
 XX comprising contacting human DNA with a probe which comprises at least 10  
 XX contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 XX and (4) a method (M4) for identifying a candidate drug as a member of a  
 XX class of drugs having a characteristic effect on gene expression in a  
 XX yeast cell comprising contacting a yeast cell with a candidate drug and  
 XX monitoring expression in the yeast cell of at least 1 NORF gene whose  
 XX expression is affected by the class of drugs. The NORF genes may be used  
 XX to study, monitor and affect phases of the cell cycle, the differentially  
 XX expressed genes may be used as markers of phases of the cell cycle. The  
 XX methods may be used to identify candidate drugs which affect the cell  
 XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 XX represent SAGE tags used in the exemplification of the present invention.  
 XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 XX method, in the exemplification of the present invention  
 XX Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
 XX  
 XX Query Match 25.0%; Score 7; DB 1; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 19 GGAGTCC 25  
 XX |||||  
 XX Db 2 GGAGTCC 8  
 XX  
 XX RESULT 637  
 XX AAF36719  
 XX ID AAF36719 standard; DNA; 10 BP.  
 XX AC AAF36719;  
 XX XX 23-MAR-2001 (first entry)  
 XX DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3458.  
 XX DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 XX KW serial analysis of gene expression; antifungal; tag; identification;  
 XX KW linker; PCR primer; ds.  
 XX OS Saccharomyces cerevisiae.  
 XX OS

PN WO200077214-A2.  
 XX 21-DEC-2000.  
 XX 14-JUN-2000; 2000WO-US016223.  
 XX 16-JUN-1999; 99US-00335032.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 XX gene expression (SAGE) tags, useful for studying, monitoring and  
 XX affecting phases of the cell cycle.  
 XX Example; Page 123; 419pp; English.  
 XX The present invention describes an isolated DNA molecule comprising a  
 XX coding sequence of a yeast gene selected from a group of 745 NORF (not  
 XX previously assigned open reading frame; or nonannotated ORF) genes  
 XX comprising a SAGE (serial analysis of gene expression) tag. Also  
 XX described are: (1) a method (M1) of using NORF genes to affect the cell  
 XX cycle comprising administering a NORF gene whose expression varies by at  
 XX least 10% between any two phases of the cell cycle selected from log  
 XX phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 XX antifungal drugs comprising: (a) contacting a test substance with a yeast  
 XX cell; and (b) monitoring expression of a NORF gene whose expression  
 XX varies as in M1, where a test substance which modifies the expression of  
 XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 XX identifying human genes which are involved in cell cycle progression  
 XX comprising contacting human DNA with a probe which comprises at least 10  
 XX contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 XX and (4) a method (M4) for identifying a candidate drug as a member of a  
 XX class of drugs having a characteristic effect on gene expression in a  
 XX yeast cell comprising contacting a yeast cell with a candidate drug and  
 XX monitoring expression in the yeast cell of at least 1 NORF gene whose  
 XX expression is affected by the class of drugs. The NORF genes may be used  
 XX to study, monitor and affect phases of the cell cycle, the differentially  
 XX expressed genes may be used as markers of phases of the cell cycle. The  
 XX methods may be used to identify candidate drugs which affect the cell  
 XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 XX represent SAGE tags used in the exemplification of the present invention.  
 XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 XX method, in the exemplification of the present invention  
 XX Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;  
 XX  
 XX Query Match 25.0%; Score 7; DB 1; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 2 GGGCCCT 8  
 XX |||||  
 XX Db 3 GGGCCCT 9  
 XX  
 XX RESULT 638  
 XX ABQ86579/c  
 XX ID ABQ86579 standard; cDNA; 11 BP.  
 XX AC ABQ86579;  
 XX DT 10-SEP-2002 (first entry)  
 XX DE Human skin stress/ageing related EST SEQ ID NO 334.  
 XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.  
 XX OS Homo sapiens.  
 XX OS

PN WO200253773-A2.  
 XX 11-JUL-2002.  
 XX  
 XX 20-DEC-2001; 2001WO-EP015178.  
 XX  
 XX 03-JAN-2001; 2001DE-01000121.  
 XX (HENK ) HENKEL KGAA.  
 XX PA  
 XX Petersohn D, Conradt M, Hofmann K;  
 XX WPI; 2002-528865/56.  
 XX  
 XX Identifying genes involved in skin stress and aging, useful e.g. in  
 PT screening for cosmetic or therapeutic agents, based on differential gene  
 PT expression.  
 XX  
 XX Claim 8; Page 50; 325pp; German.  
 XX  
 XX The invention relates to identifying (M1) genes in vitro that, in humans  
 CC or animals, are important for skin ageing and/or skin stress by serial  
 CC analysis of gene expression between mixtures of transcribed and  
 CC optionally translated, genetically encoded factors (A) obtained from  
 CC young and aged skin, to identify that genes that show strong differential  
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is  
 CC useful for: identifying markers of skin ageing and/or stress; determining  
 CC skin ageing and/or stress; and identifying or determining the effects of  
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present  
 CC sequence is one of a group of human skin ageing/stress related expressed  
 CC sequence tags (ABQ86246-ABQ87680) of the invention  
 XX  
 XX Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 25.0%; Score 7; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 19 GGAGTCC 25  
 Db 9 GGAGTCC 3  
 |||||  
 RESULT 639  
 ABV64991/C  
 ID ABV64991 standard; cDNA; 11 BP.  
 AC  
 AC ABV64991;  
 XX  
 XX 21-OCT-2002 (first entry)  
 XX Human skin EST 2777.  
 XX  
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;  
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200253774-A2.  
 PN  
 XX 11-JUL-2002.  
 PD  
 XX 20-DEC-2001; 2001WO-EP015179.  
 XX  
 XX 03-JAN-2001; 2001DE-01000127.  
 XX (HENK ) HENKEL KGAA.  
 XX PA  
 XX Petersohn D, Conradt M, Hofmann K;  
 PI WPI; 2002-590638/63.  
 XX  
 XX

PT In vitro identification of skin-expressed genes, useful for determining  
 PT homeostasis and identifying cosmetic or pharmaceutical agents against  
 XX e.g. skin cancer.  
 XX  
 XX Disclosure; Page 102; 1345pp; German.  
 XX  
 XX The invention relates to in vitro identification (M1) of genes expressed  
 CC in the skin of humans or animals by subjecting a mixture of genetically  
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
 CC so as to identify skin-expressed genes and quantify their expression.  
 CC (M1) is useful for identifying genes involved in skin homeostasis; to  
 CC determine skin homeostasis and to test agent (A) that maintains or  
 CC promotes skin homeostasis or that can be used for treating skin  
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
 CC skin. The present sequence is that of a human expressed sequence tag  
 CC (EST) of the invention  
 XX  
 XX Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 25.0%; Score 7; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 19 GGAGTCC 25  
 Db 9 GGAGTCC 3  
 |||||  
 RESULT 640  
 AAZ90850  
 ID AAZ90850 standard; DNA; 15 BP.  
 XX  
 XX AAZ90850;  
 AC  
 XX 24-MAY-2000 (first entry)  
 DT  
 XX Human NR8 gene probe #78.  
 XX DE  
 XX Haemopoietin receptor family; NR8; antibody; diagnosis;  
 KW blood formation disorder; fusion protein; probe; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO9967290-A1.  
 PN  
 XX 29-DEC-1999.  
 PD  
 XX 23-JUN-1999; 99WO-JP003351.  
 PF  
 XX 24-JUN-1998; 98JP-00214720.  
 PR  
 XX 19-OCT-1998; 98JP-00297409.  
 PR  
 XX (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.  
 PA  
 XX Nomura H, Maeda M;  
 PI  
 XX WPI; 2000-116933/10.  
 DR  
 XX Hemopoietin receptor protein family NR8 used for diagnosis of blood  
 PT formation disorders.  
 PT  
 XX Example 1; Page 41; 176pp; Japanese.  
 PS  
 XX The invention relates to the isolation of sequences encoding human  
 CC haemopoietin receptor protein family NR8 genes. The NR8 family sequences  
 CC were initially searched for comparison on a nucleic acid database with  
 CC the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid  
 CC sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90816-  
 CC Z90925 represent specific examples of probe sequences used in the search.  
 CC Antibodies to the NR8 family proteins are used for the diagnosis of blood  
 CC formation disorders. Compounds identified as binding to the proteins are

CC used for the treatment of such disorders

XX Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 25.0%; Score 7; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25  
|||||  
Db 2 GGAGTCC 8

RESULT 641

AAZ90834  
ID AAZ90834 standard; DNA; 15 BP.

XX

AC AAZ90834;

XX

DT 24-MAY-2000 (first entry)

XX

DE Human NR8 gene probe #62.

XX

Haemopoietin receptor family; NR8; antibody; diagnosis;  
blood formation disorder; fusion protein; probe; ss.

XX

OS Homo sapiens.

XX

PN WO9967290-A1.

XX

PD 29-DEC-1999.

XX

PF 23-JUN-1999; 99WO-JP003351.

XX

PR 24-JUN-1998; 98JP-00214720.

XX

PR 19-OCT-1998; 98JP-00297409.

XX

(CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX

PI Nomura H, Maeda M;

XX

DR WPI; 2000-116933/10.

XX

Haemopoietin receptor protein family NR8 used for diagnosis of blood  
formation disorders.

XX

PS Example 1; Page 40; 176pp; Japanese.

XX

CC The invention relates to the isolation of sequences encoding human  
haemopoietin receptor protein family NR8 genes. The NR8 family sequences  
were initially searched for comparison on a nucleic acid database with  
the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid  
sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ9258-259300 and AAZ90816-  
Z90925 represent specific examples of probe sequences used in the search.  
CC Antibodies to the NR8 family proteins are used for the diagnosis of blood  
formation disorders. Compounds identified as binding to the proteins are  
used for the treatment of such disorders

XX

SQ Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 25.0%; Score 7; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25  
|||||  
Db 2 GGAGTCC 8

RESULT 642

AAZ90885

ID AAZ90885 standard; DNA; 15 BP.

XX

XX

AC AAZ90885;

XX

DT 24-MAY-2000 (first entry)

XX

DE Human NR8 gene probe #113.

XX

Haemopoietin receptor family; NR8; antibody; diagnosis;  
blood formation disorder; fusion protein; probe; ss.

XX

OS Homo sapiens.

XX

PN WO9967290-A1.

XX

PD 29-DEC-1999.

XX

PF 23-JUN-1999; 99WO-JP003351.

XX

PR 24-JUN-1998; 98JP-00214720.

XX

PR 19-OCT-1998; 98JP-00297409.

XX

(CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX

PI Nomura H, Maeda M;

XX

DR WPI; 2000-116933/10.

XX

Haemopoietin receptor protein family NR8 used for diagnosis of blood  
formation disorders.

XX

PS Example 1; Page 43; 176pp; Japanese.

XX

CC The invention relates to the isolation of sequences encoding human  
haemopoietin receptor protein family NR8 genes. The NR8 family sequences  
were initially searched for comparison on a nucleic acid database with  
the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid  
sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ9258-259300 and AAZ90816-  
Z90925 represent specific examples of probe sequences used in the search.  
CC Antibodies to the NR8 family proteins are used for the diagnosis of blood  
formation disorders. Compounds identified as binding to the proteins are  
used for the treatment of such disorders

XX

SQ Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 25.0%; Score 7; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25  
|||||  
Db 2 GGAGTCC 8

RESULT 643

AAZ90922

ID AAZ90922 standard; DNA; 15 BP.

XX

AC AAZ90922;

XX

DT 24-MAY-2000 (first entry)

XX

DE Human NR8 gene probe #150.

XX

Haemopoietin receptor family; NR8; antibody; diagnosis;  
blood formation disorder; fusion protein; probe; ss.

XX

OS Homo sapiens.

XX

PN WO9967290-A1.

XX

PD 29-DEC-1999.

XX

PF 23-JUN-1999; 99WO-JP003351.

XX

PR 24-JUN-1998; 98JP-00214720.  
 PR 19-OCT-1998; 98JP-00297409.  
 PA (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.  
 PI Nomura H, Maeda M;  
 PI WPI; 2000-116933/10.  
 DR Hemopoietin receptor protein family NR8 used for diagnosis of blood  
 PT formation disorders.  
 PT Example 1; Page 45; 176pp; Japanese.  
 XX  
 XX The invention relates to the isolation of sequences encoding human  
 CC haemopoietin receptor protein family NR8 genes. The NR8 family sequences  
 CC were initially searched for comparison on a nucleic acid database with  
 CC the nucleic acid probe sequence TGGAGYNNNGAGY encoding the amino acid  
 CC sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90816-  
 CC Z90925 represent specific examples of probe sequences used in the search.  
 CC Antibodies to the NR8 family proteins are used for the diagnosis of blood  
 CC formation disorders. Compounds identified as binding to the proteins are  
 CC used for the treatment of such disorders  
 XX  
 XX Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 25.0%; Score 7; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 19 GGAGTCC 25  
 Db |||||  
 2 GGAGTCC 8  
 RESULT 644  
 ABL46308/C  
 ID ABL46308 standard; DNA; 17 BP.  
 XX  
 XX ABL46308;  
 XX 26-APR-2002 (first entry)  
 DT Mouse scavenger receptor class B type 1 oligonucleotide SEQ ID NO:275.  
 DE Nucleic acid accessible hybridisation site; detection; hybridisation;  
 XX characterisation; identification; nucleic acid structure; diagnosis;  
 KW PCR primer; probe; ss.  
 XX Mus sp.  
 OS Synthetic.  
 XX WO200198537-A2.  
 PN 27-DEC-2001.  
 PD 15-JUN-2001; 2001WO-US019401.  
 PF 17-JUN-2000; 2000US-0212308P.  
 PR 15-JUN-2001; 2001US-00212308.  
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 PA Lymanichev V, Allawi H, Dong F, Neri BP, Vener IT;  
 XX WPI; 2002-049698/06.  
 DR Identifying oligonucleotides hybridizing to nucleic acids containing  
 XX secondary structure, useful in clinical diagnosis, comprises identifying  
 PT primers that interact with the target to form an extension product under  
 PT amplification conditions.  
 XX Claim 48; Fig 79A; 409pp; English.

XX The present invention describes a method for identifying oligonucleotides  
 CC with desired hybridisation properties to nucleic acid targets containing  
 CC secondary structure. The method comprises amplifying a target nucleic  
 CC acid having at least one accessible and one inaccessible site. Primers  
 CC that form an extension product are identified as the oligonucleotides  
 CC which can interact with the folded target nucleic acid. Oligonucleotides  
 CC from the present invention can be used in novel detection methods for  
 CC clinical diagnostic purposes, including the detection and identification  
 CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
 CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
 CC sequences used in the exemplification of the present invention  
 XX  
 XX Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 25.0%; Score 7; DB 1; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 6.4e+02;  
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 11 GTGTACAGGAGTCC 25  
 Db |||||  
 15 GTAGACATAGGTC 1  
 RESULT 645  
 AAA11710/C  
 ID AAA11710 standard; DNA; 19 BP.  
 XX  
 XX AAA11710;  
 XX 14-JUL-2000 (first entry)  
 DT Human prostate-specific antigen PCR primer #4.  
 DE Prostate-specific antigen; PSA; detection; prostate cancer; PCR primer;  
 XX ss.  
 XX Homo sapiens.  
 OS JF2000069969-A.  
 PN 07-MAR-2000.  
 PD 28-AUG-1998; 98JP-00243419.  
 PF 28-AUG-1998; 98JP-00243419.  
 PR (HITB ) HITACHI CHEM CO LTD.  
 XX (NIID-) NIPPON IDENSHI KENKYUSHO KK.  
 PA WPI; 2000-264446/23.  
 XX A primer DNA and detection of an mRNA encoding a prostate-specific  
 PT antigen by using it.  
 XX Claim 2; Page 9; 10pp; Japanese.  
 XX This invention describes novel primers used in a method of detecting an  
 CC mRNA encoding prostate-specific antigen (PSA) in which cDNA synthesis is  
 CC carried out by using an mRNA encoding PSA contained in a sample as the  
 CC first template and then carrying out PCR using one of four described  
 CC primers to generate a second template. A further a PCR is carried out to  
 CC generate a third template. The primer DNA is used for the specific  
 CC detection of prostate cancer. The method is sensitive and specific.  
 CC AAA11707-A11710 represent the PCR primers described in the method of the  
 CC invention  
 XX  
 XX Sequence 19 BP; 4 A; 5 C; 6 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 25.0%; Score 7; DB 1; Length 19;  
 Best Local Similarity 66.7%; Pred. No. 6.5e+02;  
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 8 TACGTGTACAGGAG 22  
Db 19 TCCCTGTACCAAG 5

RESULT 646  
AAAF38150  
ID AAF38150 standard; DNA; 10 BP.  
XX  
AC AAF38150;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4889.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW Serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UWJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX  
DR WPI; 2001-061874/07.  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 174; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
XX method, in the exemplification of the present invention

QY Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;  
SQ

Query Match 24.3%; Score 6.8; DB 1; Length 10;

Best Local Similarity 80.0%; Pred. No. 4.5e+02;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TACGTGTAC 17  
Db 1 TCCCTGTACA 10

RESULT 647  
AAAF40202  
ID AAF40202 standard; DNA; 10 BP.  
XX  
AC AAF40202;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6941.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW Serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UWJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX  
DR WPI; 2001-061874/07.  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 247; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
XX method, in the exemplification of the present invention

SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 24.3%; Score 6.8; DB 1; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 4.5e+02;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 AGGAGTCCA 26  
 Db 1 ATGACTCCA 10

RESULT 648  
 ABQ86347  
 ID ABQ86347 standard; cDNA; 11 BP.  
 XX AC ABQ86347;  
 XX AC ABQ86347;  
 XX DT 10-SEP-2002 (first entry)  
 XX DE Human skin stress/ageing related EST SEQ ID NO 102.  
 XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.  
 XX KW Homo sapiens.  
 XX OS Homo sapiens.  
 XX FN WO200253773-A2.  
 XX PD 11-JUL-2002.  
 XX PF 20-DEC-2001; 2001WO-EP015178.  
 XX PR 03-JAN-2001; 2001DE-01000121.  
 XX PA (HENK ) HENKEL KGAA.  
 XX PI Petersohn D, Conradt M, Hofmann K;  
 XX DR WPI; 2002-528865/56.  
 XX DT Identifying genes involved in skin stress and aging, useful e.g. in  
 PT screening for cosmetic or therapeutic agents, based on differential gene  
 PT expression.  
 XX PS Claim 8; Page 41; 325pp; German.  
 XX CC The invention relates to identifying (M1) genes in vitro that, in humans  
 CC or animals, are important for skin ageing and/or skin stress by serial  
 CC analysis of gene expression between mixtures of transcribed and  
 CC optionally translated, genetically encoded factors (A) obtained from  
 CC young and aged skin, to identify that genes that show strong differential  
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is  
 CC useful for: identifying markers of skin ageing and/or stress; determining  
 CC skin ageing and/or stress; and identifying or determining the effects of  
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present  
 CC sequence is one of a group of human skin ageing/stress related expressed  
 CC sequence tags (ABQ86246-ABQ87680) of the invention  
 XX SQ Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 24.3%; Score 6.8; DB 1; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 5e+02;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TACGTGTACA 17  
 Db 1 TCCCTGTACA 10

RESULT 649  
 ABV68461  
 ID ABV68461 standard; cDNA; 11 BP.  
 XX AC ABV68461;

SQ Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 24.3%; Score 6.8; DB 1; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 5e+02;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TACGTGTACA 17  
 Db 1 TCCCTGTACA 10

RESULT 650  
 ABH89284/C  
 ID ABH89284 standard; DNA; 12 BP.  
 XX AC ABH89284;  
 XX DT 22-FEB-2002 (first entry)  
 XX DE Oligonucleotide primer SEQ ID NO 289277 for detecting SNP TSC0013867.  
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.  
 XX FN WO200177384-A2.  
 XX PN WO200177384-A2.  
 XX AC

21-OCT-2002 (first entry)  
 Human skin EST 6247.  
 Human; skin; dermatological; vulnary; antipeoriatic; antiseborrhaeic;  
 immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
 psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
 Homo sapiens.  
 WO200253774-A2.  
 11-JUL-2002.  
 20-DEC-2001; 2001WO-EP015179.  
 03-JAN-2001; 2001DE-01000127.  
 (HENK ) HENKEL KGAA.  
 Petersohn D, Conradt M, Hofmann K;  
 WPI; 2002-590638/53.  
 In vitro identification of skin-expressed genes, useful for determining  
 homeostasis and identifying cosmetic or pharmaceutical agents against  
 e.g. skin cancer.  
 Disclosure; Page 198; 1345pp; German.  
 The invention relates to in vitro identification (M1) of genes expressed  
 in the skin of humans or animals by subjecting a mixture of genetically  
 encoded factors from skin, to serial analysis of gene expression (SAGE)  
 so as to identify skin-expressed genes and quantify their expression.  
 (M1) is useful for identifying genes involved in skin homeostasis; to  
 determine skin homeostasis and to test agent (A) that maintains or  
 promotes skin homeostasis or that can be used for treating skin  
 disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
 ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
 rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
 skin. The present sequence is that of a human expressed sequence tag  
 (EST) of the invention  
 Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;





CC represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;  
 Query Match 24.3%; Score 6.8; DB 1; Length 12;  
 Best Local Similarity 80.0%; Pred. No. 5.5e+02;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TACGCTGATCA 17  
 |||||  
 DB 3 TACAGTACA 12

RESULT 653  
 ID AB110703  
 AC AB110703 standard; DNA; 12 BP.  
 XX AB110703;  
 XX  
 DT 22-FEB-2002 (first entry)  
 DE  
 DE Oligonucleotide primer SEQ ID NO 310676 for detecting SNP TSC0024049.  
 XX  
 XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB0000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 310676; 29pp + Sequence Listing; German.  
 XX

CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. fine  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 12 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 0 Other;  
 Query Match 24.3%; Score 6.8; DB 1; Length 12;  
 Best Local Similarity 80.0%; Pred. No. 5.5e+02;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCTACGCTGA 15  
 |||||

DB 2 CCTACGCTGA 11  
 RESULT 654  
 ID AAV11115/c  
 AC AAV11115 standard; RNA; 13 BP.  
 XX  
 XX AAV11115;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 14-JUL-1998 (first entry)  
 XX  
 DE Human ribozyme target sequence from HLA-DRB 19DRB #5.  
 XX  
 KW Ribozyme; target; human lymphocyte antigen; HLA-DRB; MHC allele;  
 KW major histocompatibility complex; cleavage; suppression; transplant;  
 KW incompatibility; autoimmune disease; juvenile diabetes;  
 KW rheumatoid arthritis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9704087-A1.  
 XX  
 PD 06-FEB-1997.  
 XX  
 PF 18-JUL-1996; 96WO-EP003173.  
 XX  
 PR 18-JUL-1995; 95EP-00111256.  
 XX  
 PA (KRUPP/) KRUPP G.  
 PA (MARG/) MARGET M.  
 PA (WEST/) WESTPHAL E.  
 PA (MUEL/) MUELLER-RUCHHOLTZ W.  
 XX  
 PI Krupp G, Marget M, Westphal E, Mueller-Ruchholtz W;  
 XX  
 DR WPI; 1997-132628/12.  
 XX  
 XX Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft  
 PT versus host reactions, to overcome blood incompatibility and to treat  
 PT autoimmune disease.  
 XX  
 PS Claim 5; Fig 1; 76pp; German.  
 XX

CC AAV10915-V11123 are target sequences for a novel ribozyme which cleaves  
 CC specific alleles from the major histocompatibility complex (MHC). This  
 CC ribozyme contains a catalytic region and a hybridisation region which is  
 CC complementary to all mRNA transcribed from vertebrate genes of a specific  
 CC family of closely related MHC alleles or to mRNA from a single MHC  
 CC allele, and is able to cleave such mRNA. The mRNA has a target region  
 CC which in case is essentially conserved in all genes of the family but  
 CC differs from genes of all other MHC alleles to such a degree that no  
 CC cleavage of mRNA transcribed from these other alleles occurs. This allows  
 CC the selective reduction or inhibition of expression of all genes of a  
 CC family or of a single gene. This ribozyme can be used for permanent or  
 CC transient suppression of expression of MHC alleles, in vivo or in vitro.  
 CC Specific applications are to prevent guest vs. host or host vs. guest  
 CC reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus  
 CC and Kell systems) and to treat autoimmune diseases such as juvenile  
 CC diabetes and rheumatoid arthritis. The use of this ribozyme avoids the  
 CC need for immunosuppressants in transplant patients. It provides very  
 CC specific reduction of particular HLA molecules that cause incompatibility  
 CC between donor and recipient. (Updated on 25-MAR-2003 to correct PA  
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX

SQ Sequence 13 BP; 4 A; 3 C; 5 G; 0 T; 1 U; 0 Other;  
 Query Match 24.3%; Score 6.8; DB 1; Length 13;  
 Best Local Similarity 80.0%; Pred. No. 5.9e+02;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 CAGGCGATCC 25  
 |||||

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic; Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 9229; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABP00010-ABP99989, ABH00010-ABH99989 and ABT00010-ABT99989 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 13 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 1 Other;

Query Match 24.3%; Score 6.8; DB 1; Length 13;  
Best Local Similarity 80.0%; Pred. No. 5.9e+02;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 8 TACGTGTACA 17  
DB 12 TACACGTACA 3

RESULT 657  
ID AAA26121/c  
ID AAA26121 standard; DNA; 14 BP.  
AC AAA26121;  
AC AC  
19-JUL-2000 (first entry)  
DE Oestrogen receptor hairpin ribozyme target sequence SEQ ID NO:2619.  
DE DE  
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
KW gene expression modification; cancer; phosphorothioate; endonuclease;  
KW anticancer; breast cancer; endometrium cancer; ss.  
XX Homo sapiens.  
OS OS  
WO9954459-A2.  
PN PN  
28-OCT-1999.  
PD PD  
19-APR-1999; 99WO-US008547.  
PF PF  
XX XX

PR 20-APR-1998; 98US-0082404P.  
 PR 23-JUN-1998; 98US-00103636.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Beillon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;  
 PI Matulic-Adamic J;  
 XX  
 DR WPI; 2000-013248/01.  
 XX  
 XX New nucleic acids that interact, and optionally cleave, target sequences,  
 PT used to treat cancer.  
 XX  
 PS Claim 79; Page 98; 148pp; English.  
 XX  
 CC The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphorodithioate  
 CC link, having endonuclease activity. (A), and more generally any catalytic  
 CC nucleic acid (A') that modulates expression of the oestrogen receptor  
 CC gene, are used to treat cancer (particularly of breast or endometrium),  
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype.  
 CC reagents (for RNA, in the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 14 BP; 2 A; 6 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 24.3%; Score 6.8; DB 1; Length 14;  
 Best Local Similarity 80.0%; Pred. No. 6.2e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 13 GTACAGGGAG 22  
 Db 14 GTACACGGCG 5  
 |||||  
 |||||  
 RESULT 658  
 AAQ83430  
 ID AAQ83430 standard; DNA; 14 BP.  
 XX  
 AC AAQ83430;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-SEP-1995 (first entry)  
 XX  
 DE C-fos antisense oligonucleotide.  
 XX  
 KW c-Jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense;  
 KW phosphorothioate; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN WO9502051-A2.  
 XX  
 PD 19-JAN-1995.  
 XX  
 PE 06-JUL-1994; 94WO-EP002218.  
 XX  
 PR 10-JUL-1993; 93EP-00111059.  
 XX  
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen G, Schlingensiepen R, Schlingensiepen K, Brysch W;  
 PI WPI; 1995-066896/09.  
 XX  
 DR Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and  
 PT treating neuronal injury, degeneration, cell death and/or neoplasms.  
 XX  
 XX Claim 2; Page 65; 86pp; English.  
 PS  
 XX Antisense nucleic acid hybridising with an area of the mRNA and/or DNA  
 CC comprising the genes c-jun, jun-B or c-fos, expression of which plays a  
 CC causal role in neuronal injury, degeneration, cell death and/or  
 CC neoplasms, can be used to prevent and treat such conditions. c-jun  
 CC antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B  
 CC antisense sequences are described in AAQ83322-63 and AAQ83444-45; and c-  
 CC fos antisense sequences are described in AAQ83364-439 and AAQ83446- 51.  
 CC Preferably the antisense sequences are phosphorothioate oligonucleotides  
 CC since these are not destroyed as fast by endogenous factors as naturally  
 CC occurring molecules. (Updated on 25-MAR-2003 to correct FN field.)  
 XX  
 SQ Sequence 14 BP; 4 A; 3 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 24.3%; Score 6.8; DB 1; Length 14;  
 Best Local Similarity 80.0%; Pred. No. 6.2e+02;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 11 GTGTACAGGG 20  
 Db 4 GTATACAGAG 13  
 |||||  
 |||||  
 RESULT 659  
 ABJ39464/C  
 ID ABL39464 standard; DNA; 15 BP.  
 XX  
 AC ABL39464;  
 XX  
 DT 22-APR-2002 (first entry)  
 XX  
 DE Human ETVB allele-specific oligonucleotide primer 24.  
 XX  
 KW Human; electron-transfer flavoprotein beta polypeptide; ETVB;  
 KW electron acceptor; mitochondrial matrix; glutaric acidemia type II;  
 KW novel polymorphic site; novel polymorphism; ETVB genotype; ss; GAI1;  
 KW ETVB haplotype; transgenic animal; primer; probe; chromosome 19q13;  
 KW primer-extension oligonucleotide; single nucleotide polymorphism; SNP.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WC200202580-A2.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 05-JUL-2001; 2001WO-US021306.  
 PF  
 PR 05-JUL-2000; 2000US-0215984P.  
 PR  
 XX (GENA-) GENAISANCE PHARM INC.  
 PA  
 XX Bentivegna SC, Bieglecki KM, Kazemi A, Koshy B;  
 PI WPI; 2002-154722/20.  
 XX  
 XX Novel isolated human electron-transfer-flavoprotein, beta polynucleotide,  
 PT useful for therapeutic purposes, for studying the expression and function  
 PT of the polynucleotide, and for expressing the flavoprotein.  
 XX  
 XX Claim 17; Page 14; 143pp; English.  
 PS  
 XX The invention comprises DNA, cDNA and protein sequences of the human  
 CC electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on  
 CC chromosome 19q13.3-13.4). The invention specifically relates to the

identification of 27 novel polymorphic sites within the E7FB gene.  
 Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor for nine primary flavoprotein dehydrogenases and is located in the mitochondrial matrix. ETF is composed of an alpha (E7FA) and a beta (E7FB) subunit. Electrons accepted by ETF are transferred to the mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).  
 Deficiency of ETF or ETFDH leads to glutaric acidemia type II (GAI). Therefore ETF is a pharmaceutically-important gene in the treatment of GAI. The novel ETF polymorphisms identified in the treatment of GAI for genotyping and haplotyping the ETF gene of an individual. The ETF protein and nucleic acids of the invention are useful for studying the expression and function of ETF in vivo. The ETF protein and nucleic acids are also useful for testing the efficacy of therapeutic agents and compounds for glutaric acidemia type II. The nucleic acids of the invention are useful in the production of a transgenic animal expressing the E7FB gene. Nucleic acids ABL39414-ABL39440 represent claimed ETFB allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed ETFB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548 represent claimed ETFB primer-extension oligonucleotides

Sequence 15 BP; 3 A; 5 C; 5 G; 1 T; 0 U; 1 Other;

Query Match 24.3%; Score 6.8; DB 1; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28  
 |||||  
 Db 10 GGACTCTCTGG 1

RESULT 660  
 ABA03963  
 ID ABA03963 standard; DNA; 15 BP.  
 AC ABA03963;  
 XX  
 XX  
 DT 19-FEB-2002 (first entry)  
 XX

Human STK11 gene polymorphism detection ASO primer SEQ ID NO:30.  
 Human; STK11; serine/threonine kinase 11; polymorphism; SNP;  
 single nucleotide polymorphism; Peutz-Jeghers Syndrome; genotyping;  
 haplotype; generic variant; haplotyping; allele-specific oligonucleotide;  
 ASO; primer; ss.  
 Homo sapiens.  
 WO200187906-A2.  
 XX  
 XX  
 PN  
 XX  
 PD 22-NOV-2001.  
 XX

17-MAY-2001; 2001WO-US016045.  
 XX  
 XX  
 PR 17-MAY-2000; 2000US-0204697P.  
 XX  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 XX  
 PI Bieglecki KM, Chew A, Choi JY, Nandabalan K, Sausker EA;  
 XX  
 XX  
 DR WPI; 2002-055679/07.  
 XX

Novel genetic variants of serine/threonine kinase 11 (Peutz-Jeghers syndrome) useful in studying expression and function of the protein, and for screening candidate drugs to treat diseases e.g. Peutz-Jeghers syndrome.

Claim 16; Page 13; 86pp; English.  
 The present invention describes a method for haplotyping the serine/threonine kinase 11 (Peutz-Jeghers syndrome) (STK11) gene of an individual. STK11 gene sequences can be used in gene therapy. The STK11 gene is useful for screening drug targeting comprising contacting STK11

with a candidate agent and assaying for binding activity. STK11 is useful for improving the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with STK11 activity, e.g. Peutz-Jeghers syndrome. The method is useful for haplotyping the STK11 gene in an individual, which can also be used in pharmaceutical research to validate STK11 as a candidate target for, and in design of clinical trials of candidate drugs for, treating a specific condition drugs or disease predicted to be associated with STK11 activity. Allele-specific oligonucleotides (ASOs) are useful as probes and primers for assaying a polymorphism in the target region. The present sequence represents an ASO primer used for detecting STK11 gene polymorphisms, which is used in the exemplification of the present invention

Sequence 15 BP; 2 A; 6 C; 6 G; 0 T; 0 U; 1 Other;  
 Query Match 24.3%; Score 6.8; DB 1; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 CAGGGAGTCC 25  
 |||||  
 Db 1 CACGGAGGCC 10

RESULT 661  
 AAA51767/c  
 ID AAA51767 standard; DNA; 16 BP.  
 XX  
 AC AAA51767;  
 XX  
 DT 31-OCT-2000 (first entry)  
 XX  
 DE CYP3A5 gene 5' flanking region forward sequencing primer 3A5p01.  
 XX  
 XX CYP3A5; Cytochrome P450; transcription regulatory region; polymorphism;  
 KW Activator protein-3 motif; AP-3; basic transcription element;  
 KW drug metabolism; phenotype; sequencing primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2000039332-A1.  
 XX  
 PN  
 PD 06-JUL-2000.  
 XX  
 PF 22-DEC-1999; 99WO-GB004380.  
 XX  
 PR 23-DEC-1998; 98GB-00028619.  
 XX  
 XX (JANC ) JANSSEN PHARM NV.  
 XX  
 XX Paulussen ADC, Armstrong M;  
 XX  
 FI WPI; 2000-452418/39.  
 XX  
 DR  
 XX  
 XX  
 PT Identifying subjects with a high drug metabolizing phenotype associated with cytochrome CYP3A5 expression for establishing whether a drug will be metabolized by the subject.  
 PT  
 PT Disclosure; Page 39; 68pp; English.  
 XX  
 PS  
 XX

Cytochrome P450 subfamily CYP3A5 transcription regulatory regions can be screened for the presence/absence of a polymorphic variant, preferably at positions -475 or -147 of the DNA of the 5' flanking region adjacent to the CYP3A5 coding sequence. The variants are present in an activator protein-3 (AP-3) motif and/or a basic transcription element (BTE). The polymorphisms cause increased CYP3A5 gene expression and this has been linked to drug metabolic activity. Screening for the presence of variants can be used to identify subjects with a high or low drug metabolizing phenotype associated with cytochrome CYP3A5 expression. Primers are used which in addition to hybridizing to the site of interest, are capable of introducing a restriction site which is absent in either the wild type sequence or polymorphic variants. Restriction enzyme cleavage analysis

CC can then be used to indicate the presence or absence of the variant. The  
 CC methods are used to establish, before treatment with a drug, whether the  
 CC drug will be effectively metabolized by the patient, to identify  
 CC compounds and transcription factors that can bind to a DNA sequence  
 CC encoding CYP3A5, diagnosing susceptibility to a disease which is caused  
 CC by toxins or procarcinogens metabolized by CYP3A5 and for identifying  
 CC mutagenic effects of a compound

XX Sequence 16 BP; 6 A; 3 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 24.3%; Score 6.8; DB 1; Length 16;  
 Best Local Similarity 80.0%; Pred. No. 6.6e+02;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTACGTGTAC 16  
 |||||  
 Db 11 CTCCTGTAC 2

RESULT 662  
 AAT77699  
 ID AAT77699 standard; DNA; 19 BP.

XX AC AAT77699;  
 XX DT 15-SEP-1997 (first entry)

XX DE Wheat microsatellite WMS261 left primer.

XX Microsatellite marker; hypervariable genomic fragment; Triticum aestivum;  
 KW wheat; Triticeae; sequence tagged site; STS; primer; PCR; amplif;  
 KW polymorphism; genetic analysis; hexaploid; tetraploid; mapping; ss.  
 XX Synthetic.

XX DE19525284-A1.  
 XX 02-JAN-1997.  
 XX 28-JUN-1995; 95DE-01025284.  
 XX 28-JUN-1995; 95DE-01025284.

XX (PFLA-) INST PFLANZENGENETIK & KULTURPFLANZENFOR.

XX Roeder M, Plaschke J, Ganai M;  
 XX WPI; 1997-053731/06.

XX Primers for STS microsatellite markers for wheat and related species -  
 XX useful for genetic mapping, analysis and labelling etc. of wheat.

XX Claim 5; Page 8; 8pp; German.

XX Microsatellite markers based on hypervariable genomic fragments, from  
 CC Triticum aestivum (wheat) or the tribe Triticeae, consist of a sequence  
 CC tagged site (STS), defined by 2 specific primers (of mean size 17-23  
 CC bases) that flank a microsatellite sequence at both ends, which can be  
 CC amplified to polymorphisms (PCR products of different sizes). The  
 CC microsatellites are n-fold tandem repeats (n = 10 or more) of di-, tri-,  
 CC or tetra-nucleotide sequences, combination microsatellite sequences or an  
 CC imperfect sequence in which individual bases are mutated. The  
 CC microsatellite markers can be used for genetic analysis of hexaploid and  
 CC tetraploid forms of wheat and for genetic mapping or labelling of  
 CC monogenic and polygenic properties, and for their selection; for  
 CC analysing relationships and identifying varieties; and for evaluating  
 CC varietal purity, hybrid identification and plant growth. The markers can  
 CC differentiate between almost all European wheat lines and show a higher  
 CC degree of DNA polymorphism than known probes for the wheat genome. They  
 CC can be detected by PCR, so large numbers of samples can be analysed  
 CC easily (e.g. several hundred per day). Microsatellite marker-related  
 CC polymorphisms are stably inherited so can also serve as genetic markers.  
 CC AAT77003-22 and AAT77535-716 are primer pairs that define the

CC microsatellite markers. WMS261 has a CT type repeat  
 XX Sequence 19 BP; 3 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 SQ

Query Match 24.3%; Score 6.8; DB 1; Length 19;  
 Best Local Similarity 80.0%; Pred. No. 6.7e+02;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTACGTGTAC 16  
 |||||  
 Db 1 CTCCTGTAC 10

RESULT 663  
 ADB01852/C  
 ID ADB01852 standard; DNA; 25 BP.

XX AC ADB01852;  
 XX DT 20-NOV-2003 (first entry)

XX DE Human MDZ3 scanning oligonucleotide SEQ ID 2838.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.

XX Homo sapiens.

XX EP1281758-A2.  
 XX 05-FEB-2003.  
 XX 30-JUL-2002; 2002EP-00016874.  
 XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;  
 XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in  
 XX manufacturing a medicament for treating or preventing a disorder  
 XX associated with decreased or increased expression or activity of MDZ3,  
 XX MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 2838; 103pp; English.

XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MDZ3,  
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 25 BP; 5 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 24.3%; Score 6.8; DB 1; Length 25;  
 Best Local Similarity 61.1%; Pred. No. 5.8e+02;  
 Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 CCTACGTGTACAGGAG 22  
Db 25 CACTCGCTGCACCGTAG 8

RESULT 664  
AAV11022/C  
ID AAV11022 standard; RNA; 13 BP.

Qy 9 ACGTGTACAGGA 21  
Db 13 ACTGGTACAGTA 1

RESULT 665  
AAF47953  
ID AAF47953 standard: DNA: 15 BP.

RESULT 666  
AAQ99935/c  
ID AAQ99935 standard; DNA; 16 BP.  
XX  
AC AAQ99935;  
XX  
DT 07-MAY-1996 (first entry)  
XX  
DE Human MTS1 RT-PCR primer, X2B.  
XX  
KW Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;  
KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;  
KW Gene therapy; chronic; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9525429-A1.  
XX  
PD 28-SEP-1995.  
XX  
PF 17-MAR-1995; 95WO-JS003316.  
XX  
PR 18-MAR-1994; 94US-00214581.  
PR 18-MAR-1994; 94US-00214582.  
PR 18-MAR-1994; 94US-00215088.  
PR 14-APR-1994; 94US-00227369.  
PR 01-JUN-1994; 94US-00251938.  
XX  
PA (MYRI-) MYRIAD GENETICS INC.  
XX  
PI Kamb A;  
XX  
DR WPI; 1995-344401/44.  
XX  
PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences -  
PT useful in diagnosis, prognosis and therapy of human cancer, e.g. melanoma  
PT or leukaemia.  
XX  
PS Example 12; Page 68; 156pp; English.  
XX  
CC The cDNA sequences encoding several multiple tumour suppressor (MTS)  
CC polypeptides have been isolated and sequenced, using various sequencing  
CC and amplification primers. The primer represented in this sequence was  
CC used to distinguish between two different promoters of MTS1, one alpha-  
CC specific and one beta-specific. MTS polypeptide-encoding cDNAs and  
CC mutants of these are useful for the diagnosis or prognosis of human  
CC cancer. Germ-line mutations of MTS cDNAs can be used for diagnosing  
CC predisposition to melanoma, leukaemia, astrocytoma, glioblastoma,  
CC lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers of the pancreas,  
CC thyroid, ovary, uterus, testis, kidney, stomach and rectum. The wild-type  
CC gene is useful for gene therapy and MTS polypeptides may also be used for  
CC protein replacement therapy. Also the polypeptides or cells contg. an  
CC altered MTS gene are useful for screening for potential cancer  
CC therapeutics  
XX  
SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 7e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 7 CTACGTGTACAGG 19  
Db 13 CTTCCTGGACAGC 1  
RESULT 667  
AAT00727/c  
ID AAT00727 standard; DNA; 16 BP.  
XX  
AC AAT00727;  
XX

DT 08-MAY-1996 (first entry)  
XX  
DE Multiple tumour suppressor 1 gene PCR primer.  
XX  
KW Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;  
KW predisposition; melanoma; leukaemia; lymphoma; prognosis; pancreas;  
KW breast; thyroid; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9525813-A1.  
XX  
PD 28-SEP-1995.  
XX  
PF 17-MAR-1995; 95WO-US003537.  
XX  
PR 18-MAR-1994; 94US-00214582.  
PR 18-MAR-1994; 94US-00215086.  
PR 18-MAR-1994; 94US-00215087.  
PR 14-APR-1994; 94US-00227369.  
PR 01-JUN-1994; 94US-00251938.  
XX  
PA (UTAH) UNIV UTAH RES FOUND.  
PA (MYRI-) MYRIAD GENETICS INC.  
XX  
PI Skolnick MH, Cannon-Albright LA, Kamb A;  
XX  
DR WPI; 1995-344626/44.  
XX  
PT Detecting polymorphism associated with cancer predisposition - also DNA,  
PT vectors and host cells e.g. for gene or protein replacement therapy and  
PT drug screening.  
XX  
PS Example 12; Page 68; 148pp; English.  
XX  
CC An individual can be diagnosed as having a predisposition to cancer by  
CC detecting an alteration in the wild type multiple tumour suppressor (MTS)  
CC gene, using gene probes which hybridise to the MTS1 gene exon 1 or exon  
CC 1beta (amplified using the PCR primers AAT00724-27). The above assay can  
CC also be used in the diagnosis and prognosis of melanoma, lymphoma,  
CC leukaemia and pancreas, breast and thyroid cancers, etc  
XX  
SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 7e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 7 CTACGTGTACAGG 19  
Db 13 CTTCCTGGACAGC 1  
RESULT 668  
AAT69788/c  
ID AAT69788 standard; DNA; 16 BP.  
XX  
AC AAT69788;  
XX  
DT 25-MAR-2003 (revised)  
DT 10-SEP-1997 (first entry)  
XX  
DE P16 promoter primer X2B.  
XX  
KW Primer; polymerase chain reaction; PCR; amplification; P16; promoter; ss.  
OS Synthetic.  
XX  
PN US5624819-A.  
XX  
PD 29-APR-1997.  
XX  
PF 07-JUN-1995; 95US-00474177.

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XX PR 18-MAR-1994; 94US-00214582.
XX PR 18-MAR-1994; 94US-00215086.
XX PR 18-MAR-1994; 94US-00215086.
XX PR 14-APR-1994; 94US-00227369.
XX PR 01-JUN-1994; 94US-00251938.
XX PR 17-MAR-1995; 95WO-US0003537.
XX PA (MYRI-) MYRIAD GENETICS INC.
XX PA (UTAH) UNIV UTAH RES FOUND.
XX PI Cannon-Albright LA, Kamb A, Skolnick MH;
XX DR WPI; 1997-258217/23.
XX SQ Human mutant multiple tumour suppressor gene sequences - for production
XX PT of recombinant mutant polypeptide(s).
XX FS Example 12; Col 81-82; 72pp; English.
XX XX The present sequence is primer for the PCR amplification of the P16
XX CC promoter. (Updated on 25-MAR-2003 to correct PF field.)
XX XX Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX SQ
XX Query Match 23.6%; Score 6.6; DB 1; Length 16;
XX Best Local Similarity 69.2%; Pred. No. 7e+02;
XX Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX QY 7 CTACGTGTACAGG 19
XX Db 13 CTTCCTGGACAG 1
XX RESULT 669
XX AAV53838/c
XX ID AAV53838 standard; DNA; 16 BP.
XX AC AAV53838;
XX XX 04-DEC-1998 (first entry)
XX DT Nucleotide sequence of PCR primer 9.
XX DE Multiple tumour suppressor; MTS; human; cancer; hybridisation;
XX KW somatic mutation; gene therapy; PCR; primer; amplification; ss.
XX OS Synthetic.
XX OS US5801236-A.
XX FN 01-SEP-1998.
XX PD 07-JUN-1995; 95US-00480810.
XX EF 18-MAR-1994; 94US-00214582.
XX XX 18-MAR-1994; 94US-00215086.
XX PR 18-MAR-1994; 94US-00215087.
XX PR 14-APR-1994; 94US-00227369.
XX PR 01-JUN-1994; 94US-00251938.
XX PR 17-MAR-1995; 95WO-US0003537.
XX XX (MYRI-) MYRIAD GENETICS INC.
XX PA Kamb A;
XX XX WPI; 1998-494842/42.
XX XX Nucleic acids based on multiple tumour suppressor, MTS, sequences -
XX PT useful as hybridisation probes, primers and recombinant production of MTS
XX PT in the diagnosis and treatment of cancers related to MTS mutation(s).
XX XX Example 12; Col 51; 73pp; English.
XX PS

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XX CC This is the nucleotide sequence of a PCR primer used for amplification in
XX CC the method of the invention involving the use of the multiple tumour
XX CC suppressor (MTS) gene, to diagnose and treat cancer. The MTS gene is
XX CC useful in the diagnosis and prognosis of human cancer, e.g. by standard
XX CC nucleic hybridisation techniques of patient samples. The mutated
XX CC sequences are those that are present in somatic mutations of the gene in
XX CC cancers. The vectors can be used for gene therapy strategies to replace
XX CC function of mutated protein in patients. These can also be used to
XX CC construct protein mimetics, also for therapeutic strategies. In addition
XX CC the expression constructs can also be used for recombinant production of
XX CC MTS. Recombinant MTS can be used to screen for drugs to be used for
XX CC cancer therapy, and the protein itself may also be used to restore MTS
XX CC function in a cell
XX SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX Query Match 23.6%; Score 6.6; DB 1; Length 16;
XX Best Local Similarity 69.2%; Pred. No. 7e+02;
XX Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX QY 7 CTACGTGTACAGG 19
XX Db 13 CTTCCTGGACAG 1
XX RESULT 670
XX AAV11257/c
XX ID AAV11257 standard; DNA; 16 BP.
XX AC AAV11257;
XX XX 15-JUL-1998 (first entry)
XX DT Human MTS1 and MTS1E1-beta PCR primer X2B.
XX DE MTS1; MTS2; multiple tumour suppressor; diagnosis; cancer;
XX KW germ-line mutation; familial melanoma locus; MLM; predisposition; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX XX US5739027-A.
XX PN 14-APR-1998.
XX PD 07-JUN-1995; 95US-00487033.
XX PF 18-MAR-1994; 94US-00214582.
XX PR 18-MAR-1994; 94US-00215086.
XX PR 18-MAR-1994; 94US-00215087.
XX PR 14-APR-1994; 94US-00227369.
XX PR 01-JUN-1994; 94US-00251938.
XX PR 17-MAR-1995; 95WO-US0003537.
XX XX (MYRI-) MYRIAD GENETICS INC.
XX PA Kamb A;
XX XX WPI; 1998-250421/22.
XX DR DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are useful
XX PT for the diagnosis of cancers related to MTS1E1-beta mutation(s) and their
XX PT treatment.
XX XX Example 12; Col 81-82; 72pp; English.
XX PS
XX CC Primers AAV11256 and AAV11257 are used in the isolation of the human
XX CC multiple tumour suppressor proteins, MTS1 and MTS1E1-beta. The MTS gene
XX CC locus is also referred to as the familial melanoma (MLM) gene locus,
XX CC located on human chromosome 9p21. Germ line mutations in MTS genes can be
XX CC used in the diagnosis of predisposition to cancers, e.g. melanoma,
XX CC leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's

```





therapy; MTS1elbeta; PCR primer; ss.  
 KW XX  
 OS XX  
 XX XX  
 FN US5989815-A.  
 XX XX  
 PD 23-NOV-1999.  
 XX XX  
 FF 29-APR-1997; 97US-00848251.  
 XX XX  
 PR 18-MAR-1994; 94US-00214582.  
 PR 18-MAR-1994; 94US-00215086.  
 PR 18-MAR-1994; 94US-00215087.  
 PR 14-APR-1994; 94US-00227369.  
 PR 01-JUN-1994; 94US-00251938.  
 PR 17-MAR-1995; 95WO-US003537.  
 PR 07-JUN-1995; 95US-00474083.  
 XX XX  
 PA (UTAH ) UNIV UTAH RES FOUND.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX XX  
 PI Skolnick MH, Cannon-Albright LA, Kamb A;  
 XX XX  
 XX WPI; 2000-070785/06.  
 DR XX  
 XX  
 XX Diagnosing a polymorphism associated with a predisposition for cancer.  
 XX XX  
 PS Example 12; Col 48; 74pp; English.  
 XX XX  
 CC This sequence is a PCR primer for DNA encoding human MTS1elbeta. The  
 CC invention relates to a method for diagnosing a polymorphism associated  
 CC with a predisposition to cancer by detecting a germ-line alteration of a  
 CC wild-type Multiple Tumour Suppressor (MTS) gene or its expression  
 CC products in a human sample. The method comprises detecting a germ-line  
 CC alteration of a wild-type MTS gene or its expression products in a human  
 CC sample, the alteration indicating a predisposition to at least one of the  
 CC cancers. The cancer is selected from melanoma, leukaemia, astrocytoma,  
 CC glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, chronic lymphocytic  
 CC leukaemia (CLL), and cancers of the pancreas, breast, thyroid, ovary,  
 CC uterus, testis, kidney, stomach and rectum. The method may be used as  
 CC basis for developing very important diagnostic tests capable of  
 CC predicting the predisposition to cancer. The MTS gene is involved in the  
 CC progression of multiple tumour types and may provide means for a general  
 CC anti-cancer therapy by virtue of its ability to suppress tumour growth  
 XX XX  
 SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
 Query Match 23.6%; Score 6.6; DB 1; Length 16;  
 Best Local Similarity 69.2%; Pred. No. 7e+02;  
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 7 CTACGTTACAGG 19  
 DB 13 CTTCCTGGACAG 1  
 RESULT 674  
 AAZ39993/c  
 ID AAZ39993 standard; DNA; 16 BP.  
 XX XX  
 AC AAZ39993;  
 XX XX  
 DT 11-FEB-2000 (first entry)  
 XX XX  
 DE PCR primer for human multiple tumour suppressor 1 coding sequence.  
 XX XX  
 KW Multiple tumour suppressor; MTS; human; diagnosis; Hodgkin's lymphoma;  
 KW cancer predisposition; melanoma; leukaemia; lymphoma; glioma; MTS1;  
 KW PCR primer; ss.  
 XX XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX XX

US5994095-A.  
 PN XX  
 PD 30-NOV-1999.  
 XX XX  
 FF 07-JUN-1995; 95US-00486047.  
 XX XX  
 PR 18-MAR-1994; 94US-00214582.  
 PR 18-MAR-1994; 94US-00215086.  
 PR 18-MAR-1994; 94US-00215087.  
 PR 14-APR-1994; 94US-00227369.  
 PR 01-JUN-1994; 94US-00251938.  
 PR 17-MAR-1995; 95WO-US003316.  
 XX XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX XX  
 PI Kamb A;  
 XX XX  
 DR WPI; 2000-038259/03.  
 XX XX  
 PT Multiple tumor suppressor cDNA, useful for diagnosing or determining a  
 PT predisposition to cancer.  
 XX XX  
 PS Example 12; Col 48; 72pp; English.  
 XX XX  
 CC This sequence represents a PCR primer for the human multiple tumour  
 CC suppressor 1 (MTS1) coding sequence. The invention relates to the human  
 CC MTS2 DNA and protein sequences. The DNA sequences are useful for  
 CC diagnosing or determining a predisposition to cancers e.g. melanoma,  
 CC leukaemia, lymphoma, glioma, Hodgkin's lymphoma and cancers of the  
 CC pancreas, breast, thyroid, ovary, kidney, uterus and stomach  
 XX XX  
 SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
 Query Match 23.6%; Score 6.6; DB 1; Length 16;  
 Best Local Similarity 69.2%; Pred. No. 7e+02;  
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 7 CTACGTTACAGG 19  
 DB 13 CTTCCTGGACAG 1  
 RESULT 675  
 AA39372/c  
 ID AAA39372 standard; DNA; 16 BP.  
 XX XX  
 AC AAA39372;  
 XX XX  
 DT 12-SEP-2000 (first entry)  
 XX XX  
 DE Human P16 PCR primer SEQ ID NO:23.  
 XX XX  
 KW Human; multiple tumour suppressor; MTS; somatic mutation; cancer;  
 KW diagnosis; germ line mutation; gene therapy; cytostatic; melanoma;  
 KW leukaemia; astrocytoma; glioblastoma; lymphoma; glioma;  
 KW Hodgkin's lymphoma; PCR primer; ss.  
 XX XX  
 OS Homo sapiens.  
 XX XX  
 PN US6060301-A.  
 XX XX  
 PD 09-MAY-2000.  
 XX XX  
 FF 14-JUL-1998; 98US-00115252.  
 XX XX  
 PR 18-MAR-1994; 94US-00214582.  
 PR 18-MAR-1994; 94US-00215086.  
 PR 18-MAR-1994; 94US-00215087.  
 PR 14-APR-1994; 94US-00227369.  
 PR 01-JUN-1994; 94US-00251938.  
 PR 17-MAR-1995; 95WO-US003316.  
 PR 07-JUN-1995; 95US-00480810.  
 PR 08-DEC-1997; 97US-00986147.

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XX PA (MYRI-) MYRIAD GENETICS INC.
XX PI Kamb A;
XX DR WPI; 2000-349676/30.
XX XX
XX PT New vector useful for gene therapy of cancer associated with mutation in
XX PT tumor suppressor gene, comprises DNA sequence of multiple tumor
XX PT suppressor gene.
XX XX
XX PS Example 12; Col 48; 71pp; English.
XX XX
XX CC The present invention describes a vector (I) comprising an isolated DNA
XX CC sequence of a multiple tumour suppressor (MTS) gene having a
XX CC polynucleotide sequence of the human MTS1E1-beta. (I) is useful for
XX CC introducing wild-type MTS function to a cancerous or pre-cancerous cell
XX CC which carries diminished or mutant MTS alleles for suppressing neoplastic
XX CC growth of the recipient cells. (I) is also useful for increasing the
XX CC level of expression of MTS gene even in tumour cells in which the mutant
XX CC gene is expressed at a normal level but the gene product is not fully
XX CC functional. A host cell transformed with (I) is useful as a model system
XX CC to study cancer remission and drug treatment which promotes such
XX CC remission. The present invention relates to somatic mutations and germ
XX CC line mutations in the MTS gene and their use in the diagnosis and
XX CC prognosis of human cancer e.g. melanoma, leukaemia, astrocytoma,
XX CC glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, and cancers of the
XX CC pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and
XX CC rectum. The present sequence represents a PCR primer used in an example
XX CC from the present invention
XX XX
XX SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 CTACGTGTACAGG 19
Db 13 CTTCTGGACAGC 1

RESULT 676
AAFI186/c
ID AAFI186 standard; DNA; 16 BP.
XX AC AAFI186;
XX AC 23-APR-2001 (first entry)
XX DT
XX DE Primer #13.
XX XX Human; multiple tumour suppressor; MTS; cancer; gene therapy; ss.
XX OS Homo sapiens.
XX XX US6180776-B1.
XX PN 30-JAN-2001.
XX PD
XX XX 22-JUL-1998; 98US-00120129.
XX PF
XX XX 18-MAR-1994; 94US-00214582.
XX PR 18-MAR-1994; 94US-00215086.
XX PR 18-MAR-1994; 94US-00215087.
XX PR 01-JUN-1994; 94US-00251938.
XX PR 17-MAR-1995; 95WO-US003316.
XX PR 07-JUN-1995; 95US-00486047.
XX XX (MYRI-) MYRIAD GENETICS INC.
XX XX Kamb A;
XX XX WPI; 2001-158668/16.
XX XX
XX PT Novel multiple tumor suppressor gene useful for diagnosing, prognosing
XX PT and treating cancers, such as melanoma, leukemia, glioblastoma and
XX PT Hodgkin's lymphoma.
XX XX
XX PS Example 12; Col 48; 71pp; English.
XX XX
XX CC The present invention relates to human multiple tumor suppressor-2 (MTS2)

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AC AAC83090;  
 XX 23-FEB-2001 (first entry)  
 DT Primer X2B used in the invention.  
 DE MTS, Multiple Tumour Suppressor; cancer; antibody; ss.  
 XX Homo sapiens.  
 OS  
 XX US6140473-A.  
 PN 31-OCT-2000.  
 XX 22-JUL-1998; 98US-00120128.  
 XX 18-MAR-1994; 94US-00214582.  
 PR 18-MAR-1994; 94US-00215086.  
 PR 18-MAR-1994; 94US-00215087.  
 PR 14-APR-1994; 94US-00227369.  
 PR 01-JUN-1994; 94US-00251938.  
 PR 17-MAR-1995; 95WO-US003316.  
 PR 07-JUN-1995; 95US-00486047.  
 XX (MYRI-) MYRIAD GENETICS INC.  
 PA Kamb A;  
 XX WPI; 2001-014867/02.  
 DR New multiple tumor suppressor 2-specific antibodies useful for detecting  
 PT differences in the absence of the peptides or mutant gene products, or  
 PT for screening tissues.  
 XX Example 12; Col 48; 71pp; English.  
 XX The present invention relates to an antibody or its fragment that  
 CC specifically binds to a human multiple tumour suppressor (MTS). The  
 CC invention is useful for detecting differences in the absence of MTS  
 CC peptides, to screen a tissue or to detect mutant MTS gene products. The  
 CC antibodies will immunoprecipitate MTS proteins from solution as well as  
 CC react with MTS protein on Western or immunoblots of polyacrylamide gels  
 XX Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 23.6%; Score 6.6; DB 1; Length 16;  
 Best Local Similarity 69.2%; Pred. No. 7e+02; 4; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0;  
 QY 7 CTACGTTGTACAGG 19  
 DB 13 CTTCTGGACACG 1  
 RESULT 681  
 AA279758  
 ID AA279758 standard; DNA; 10 BP.  
 XX AAZ79758;  
 AC AAZ79758;  
 XX 10-APR-2000 (first entry)  
 DT Human breast tumour downregulated gene SAGE tag, SEQ ID NO:49.  
 XX SAGE tag; serial analysis of gene expression; diagnosis;  
 KW differential gene expression; characterisation; targeted expression;  
 KW tumour; cancer; immunotherapy; ss.  
 XX Homo sapiens.  
 OS  
 XX WO9966303-A2.  
 PN 23-DEC-1999.  
 PD

XX 17-JUN-1999; 99WO-US013820.  
 PF 19-JUN-1998; 98US-0089833P.  
 XX 19-JUN-1998; 98US-0089844P.  
 PR 19-JUN-1998; 98US-0089853P.  
 PR 19-JUN-1998; 98US-0089878P.  
 PR 19-JUN-1998; 98US-008991P.  
 PR 19-JUN-1998; 98US-008992P.  
 PR 19-JUN-1998; 98US-008993P.  
 PR 19-JUN-1998; 98US-008994P.  
 PR 19-JUN-1998; 98US-008997P.  
 PR 19-JUN-1998; 98US-008999P.  
 PR 19-JUN-1998; 98US-009000P.  
 PR 19-JUN-1998; 98US-009003P.  
 PR 19-JUN-1998; 98US-0090036P.  
 PR 19-JUN-1998; 98US-0090039P.  
 PR 19-JUN-1998; 98US-0090040P.  
 PR 19-JUN-1998; 98US-0090041P.  
 PR 19-JUN-1998; 98US-0090042P.  
 PR 19-JUN-1998; 98US-0090043P.  
 PR 19-JUN-1998; 98US-0090044P.  
 PR 19-JUN-1998; 98US-0090045P.  
 PR 19-JUN-1998; 98US-0090047P.  
 PR 19-JUN-1998; 98US-0090048P.  
 PR 19-JUN-1998; 98US-0090072P.  
 PR 19-JUN-1998; 98US-0090076P.  
 PR 19-JUN-1998; 98US-0090077P.  
 PR 19-JUN-1998; 98US-0090078P.  
 PR 19-JUN-1998; 98US-0090079P.  
 PR 19-JUN-1998; 98US-0090080P.  
 PR 08-DEC-1998; 98US-0111715P.  
 XX (GENZ ) GENZYME CORP.  
 PA (ROBE) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.  
 XX Roberts BL, Shankara S;  
 PI WPI; 2000-106132/09.  
 DR New polynucleotide useful in cancer immunotherapy.  
 XX Claim 1; Page 54; 97pp; English.  
 XX Sequences AAZ79710-279916 represent SAGE (serial analysis of gene  
 CC expression) tags used to identify mRNA transcripts which are  
 CC differentially expressed in a variety of normal or malignant cell types.  
 CC Some of the transcripts correspond to known genes or ESTs (expressed  
 CC sequence tags) which were previously unknown to be preferentially or  
 CC differentially expressed in that particular cell type, while other  
 CC transcripts correspond to novel genes. The invention also provides a  
 CC nucleotide comprising a promoter sequence derived from one of the  
 CC differentially expressed genes, which may optionally be operably linked  
 CC to a foreign nucleotide sequence, and gene delivery vehicles and host  
 CC cells comprising the polynucleotides of the invention. A nucleotide  
 CC comprising sequences AAZ79710-279916 may be used in diagnostic procedures  
 CC to characterise a cell of a specific tissue type and to determine whether  
 CC it is normal or malignant. They may be used to screen for agents that  
 CC modulate expression of differentially expressed genes compound. The  
 CC promoter/foreign gene construct of the invention may be used for  
 CC targeted expression of the foreign gene in a particular cell type. For  
 CC example, a promoter derived from a gene preferentially expressed in  
 CC dendritic cells (antigen-presenting cells, or APCs) may be operably  
 CC linked to a sequence encoding an immunostimulatory molecule and a  
 CC sequence encoding an antigen. Such a construct could be transduced into  
 CC APCs and would be useful for inducing an immune response by educating  
 CC immune effector cells in vivo, or in cancer immunotherapy  
 XX Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 22.9%; Score 6.4; DB 1; Length 10;  
 Best Local Similarity 87.5%; Pred. No. 5.4e+02;

CC gene. The invention is useful for diagnosing, prognosing and treating  
CC cancers. It is also useful for screening drugs for cancer therapy and  
CC gene therapy  
XX  
SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 7e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 7 CTACGTGTACAGG 19  
Db 13 CTTCCTGGACAGC 1  
RESULT 678  
ID AAS02583/c  
XX AAS02583 standard; DNA; 16 BP.  
XX AAS02583;  
AC AAS02583;  
XX  
DT 29-AUG-2001 (first entry)  
XX  
DE PCR primer X2B used in analysis of multiple tumour suppressor MTS1/2.  
XX  
KW Human; multiple tumour suppressor; MTS1; MTS2; therapeutic; diagnostic;  
KW cancer; gene therapy; melanoma; leukaemia; astrocytoma; glioblastoma;  
KW lymphoma; glioma; Hodgkin's lymphoma; chronic lymphatic leukaemia;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6210949-B1.  
XX  
XX US6210949-B1.  
PD 03-APR-2001.  
XX  
XX 30-NOV-1998; 98US-00201139.  
XX  
XX 17-MAR-1995; 95WO-0003316.  
PR 07-JUN-1995; 95US-00487033.  
XX 28-JUL-1995; 95US-00508735.  
XX  
XX (MYRI-) MYRIAD GENETICS INC.  
PA  
PI Stone S, Jiang P, Kamb A;  
XX  
XX WPI; 2001-280859/29.  
DR  
XX  
PT New mouse multiple tumor suppressor gene, useful for diagnosing or  
PT prognosing human cancer or as gene therapy for treating cancer,  
PT particularly melanoma, leukemia, astrocytoma, lymphoma or cancers of the  
PT pancreas or breast.  
XX  
XX Example 13; Col 51; 80pp; English.  
PS  
XX The sequence represents PCR primer X2B used in analysis of multiple  
CC tumour suppressor MTS1 and MTS2. The MTS genes, and expression products,  
CC are useful for treating, diagnosing or prognosing human cancer. In  
CC particular, the MTS gene is useful for diagnosing a predisposition to or  
CC as a gene therapy for melanoma, leukaemia, astrocytoma, glioblastoma,  
CC lymphoma, glioma, Hodgkin's lymphoma, chronic lymphatic leukaemia (CLL),  
CC or cancers of the pancreas, breast, thyroid, ovary, uterus, testis,  
CC kidney, stomach or rectum. The gene may be used in both cancerous and pre  
CC -cancerous cells  
XX  
SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 7e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 7 CTACGTGTACAGG 19  
Db 13 CTTCCTGGACAGC 1

Db 13 CTTCCTGGACAGC 1  
RESULT 679  
ID AAD04711/c  
XX AAD04711 standard; DNA; 16 BP.  
XX AAD04711;  
AC AAD04711;  
XX  
DT 04-JUL-2001 (first entry)  
XX  
DE Human MTS and MTS1Elbeta sequence amplifying primer, X2B.  
XX  
KW Human; multiple tumour suppressor; MTS1Elbeta; cytostatic;  
KW germ line mutation; gene therapy; melanoma; leukaemia; astrocytoma; CLL;  
KW glioblastoma; lymphoma; glioma; Hodgkin's lymphoma; cancer; rectum;  
KW pancreas; breast; thyroid; ovary; uterus; kidney; stomach;  
KW somatic mutation; MTS; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
FN US6218146-B1.  
XX  
XX 17-APR-2001.  
PD  
XX 22-JUL-1998; 98US-00120131.  
XX  
PR 18-MAR-1994; 94US-00214582.  
PR 18-MAR-1994; 94US-00215086.  
PR 18-MAR-1994; 94US-00215087.  
PR 14-APR-1994; 94US-00227369.  
PR 01-JUN-1994; 94US-00251938.  
PR 17-MAR-1995; 95WO-US003316.  
PR 07-JUN-1995; 95US-00486047.  
XX  
XX (MYRI-) MYRIAD GENETICS INC.  
PA  
PI Kamb A;  
XX  
XX WPI; 2001-289831/30.  
DR  
XX  
PT Novel multiple tumor suppressor proteins useful for diagnosis and  
PT prognosis of human cancer and for screening drugs for cancer treatment.  
XX  
XX Example 13; Col 52; 71pp; English.  
XX  
XX The invention relates to somatic and germ line mutations in the multiple  
CC tumour suppressor (MTS) gene in human cancer. The invention also relates  
CC to therapy of human cancer which have a mutation in the MTS gene,  
CC including gene therapy, protein replacement therapy, and protein  
CC mimetics. The MTS sequences are useful for diagnosing predisposition to  
CC human cancer or for diagnosing and prognosing human cancers such as  
CC melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,  
CC Hodgkin's lymphoma, CLL and cancers of pancreas, breast, thyroid, ovary,  
CC uterus, testis, kidney, stomach and rectum. They are also used for  
CC screening drugs for cancer treatment. The present sequence is primer, X2B  
CC used for amplifying human MTS and MTS1Elbeta sequence  
XX  
SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 7e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 7 CTACGTGTACAGG 19  
Db 13 CTTCCTGGACAGC 1  
RESULT 680  
ID AAC83090/c  
XX AAC83090 standard; DNA; 16 BP.  
XX

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCGTGACA 17  
| | | | |  
Db 2 CCGTGACA 9

RESULT 682  
ABV67783  
ID ABV67783 standard; cDNA; 11 BP.  
XX  
AC ABV67783;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 5569.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 179; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 1 G; 2 T; 0 U; 0 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 11;  
Best Local Similarity 87.5%; Pred. No. 6e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCGTGACA 17  
| | | | |  
Db 4 CCGTGACA 11

RESULT 683  
ABV70593/c  
ID ABV70593 standard; cDNA; 11 BP.  
XX  
AC ABV70593;  
XX

DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 8379.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Claim 24; Page 268; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 11;  
Best Local Similarity 87.5%; Pred. No. 6e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 GGAGTCCA 26  
| | | | |  
Db 8 GGATGCCA 1

RESULT 684  
ABV63172/c  
ID ABV63172 standard; cDNA; 11 BP.  
XX  
AC ABV63172;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 958.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.



CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
 CC skin. The present sequence is that of a human expressed sequence tag  
 CC (EST) of the invention  
 SQ Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 11;  
 Best Local Similarity 87.5%; Pred. No. 6e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CGTGTACA 17  
 Db 11 CCTGTACA 4

RESULT 687  
 ABH73583  
 ID ABH73583 standard; DNA; 12 BP.  
 XX AC ABH73583;  
 XX XX  
 DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 273568 for detecting SNP TSC0003234.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.

XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 273568; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 22.9%; Score 6.4; DB 1; Length 12;  
 Best Local Similarity 87.5%; Pred. No. 6.5e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGTGTA 15  
 Db 3 TACCGGTA 10

RESULT 689  
 AB116213/c  
 ID AB116213 standard; DNA; 12 BP.  
 XX AC AB116213;  
 XX XX  
 DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 316186 for detecting SNP TSC0027326.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 310578; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

RESULT 688  
 AB110705/c  
 ID AB110705 standard; DNA; 12 BP.  
 XX AC AB110705;  
 XX XX  
 DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 310678 for detecting SNP TSC0024049.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.

XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 310578; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 3 A; 4 C; 2 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 22.9%; Score 6.4; DB 1; Length 12;  
 Best Local Similarity 87.5%; Pred. No. 6.5e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGTGTA 15  
 Db 11 TACCGGTA 4

RESULT 689  
 AB116213/c  
 ID AB116213 standard; DNA; 12 BP.  
 XX AC AB116213;  
 XX XX  
 DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 316186 for detecting SNP TSC0027326.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 310578; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 3 A; 4 C; 2 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 22.9%; Score 6.4; DB 1; Length 12;  
 Best Local Similarity 87.5%; Pred. No. 6.5e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGTGTA 15  
 Db 11 TACCGGTA 4

RESULT 689  
 AB116213/c  
 ID AB116213 standard; DNA; 12 BP.  
 XX AC AB116213;  
 XX XX  
 DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 316186 for detecting SNP TSC0027326.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;



KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 FN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 316186; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 22.9%; Score 6.4; DB 1; Length 12;  
 Best Local Similarity 87.5%; Pred. No. 6.5e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 CCCTAGCT 12  
 DB 8 CCCTACTT 1  
 XX  
 RESULT 690  
 ABC49804  
 ID ABC49804 standard; DNA; 13 BP.  
 XX  
 AC ABC49804;  
 XX  
 XX 21-FEB-2002 (first entry)  
 DE  
 DE Oligonucleotide SEQ ID NO 49821 for detecting SNP TSC0014053.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX

PA (EPIG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 49821; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 1 Other;  
 XX  
 Query Match 22.9%; Score 6.4; DB 1; Length 13;  
 Best Local Similarity 87.5%; Pred. No. 6.8e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 TACGGGTA 15  
 DB 3 TACGGGTA 10  
 XX  
 RESULT 691  
 ABC49805/c  
 ID ABC49805 standard; DNA; 13 BP.  
 XX  
 AC ABC49805;  
 XX  
 XX 21-FEB-2002 (first entry)  
 DT  
 DE Oligonucleotide SEQ ID NO 49822 for detecting SNP TSC0014053.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 49822; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 4 A; 4 C; 2 G; 2 T; 0 U; 1 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 13;  
 Best Local Similarity 87.5%; Pred. No. 6.8e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGCTGA 15  
 |||||  
 Db 11 TACGCGTA 4

RESULT 692

ABC37725  
 ID ABC37725 standard; DNA; 13 BP.

XX AC ABC37725;

XX DT 20-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 37742 for detecting SNP TSC0011735.

XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.

XX Claim 1; SEQ ID NO 37742; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 3 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 13;  
 Best Local Similarity 87.5%; Pred. No. 6.8e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGCTGA 15  
 |||||  
 Db 5 TACGCGTA 12

RESULT 693

ABC37724/c  
 ID ABC37724 standard; DNA; 13 BP.

XX AC ABC37724;

XX DT 20-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 37741 for detecting SNP TSC0011735.

XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.

XX Claim 1; SEQ ID NO 37741; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 4 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 13;  
 Best Local Similarity 87.5%; Pred. No. 6.8e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGCTGA 15  
 |||||  
 Db 9 TACGCGTA 2

RESULT 694

ADB00353/c  
 ID ADB00353 standard; DNA; 17 BP.

XX AC ADB00353;  
 XX DT 20-NOV-2003 (first entry)  
 XX DE Human MD23 scanning oligonucleotide SEQ ID 1339.  
 XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 XX KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 XX KW developmental disorder; ss.  
 XX OS Homo sapiens.  
 XX PN EP1281758-A2.  
 XX PD 05-FEB-2003.  
 XX PF 30-JUL-2002; 2002EP-00016874.  
 XX PR 02-AUG-2001; 2001US-00922181.  
 XX PA (AEOM-) AEOMICA INC.  
 XX PI Shannon M, Gu Y, Nguyen C;  
 XX WIPI; 2003-423107/40.  
 XX DT 30-JUL-2002; 2002EP-00016874.  
 XX PF 02-AUG-2001; 2001US-00922181.  
 XX PR (AEOM-) AEOMICA INC.  
 XX PI Shannon M, Gu Y, Nguyen C;  
 XX WIPI; 2003-423107/40.  
 XX DT New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 XX Example 8; SEQ ID NO 1339; 103pp; English.  
 CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 22.9%; Score 6.4; DB 1; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 7.4e+02;  
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 7 CTACGTTGACAGGAG 22  
 Db 17 CTCGCTGCACACGTAG 2  
 RESULT 695  
 ADB00354/C  
 ID ADB00354 standard; DNA; 17 BP.  
 XX AC ADB00354;  
 XX DT 20-NOV-2003 (first entry)  
 XX DE Human MD23 scanning oligonucleotide SEQ ID 1340.  
 XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;

KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX OS Homo sapiens.  
 XX PN EP1281758-A2.  
 XX PD 05-FEB-2003.  
 XX PF 30-JUL-2002; 2002EP-00016874.  
 XX PR 02-AUG-2001; 2001US-00922181.  
 XX PA (AEOM-) AEOMICA INC.  
 XX PI Shannon M, Gu Y, Nguyen C;  
 XX WIPI; 2003-423107/40.  
 XX DT New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 XX Example 8; SEQ ID NO 1340; 103pp; English.  
 CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 22.9%; Score 6.4; DB 1; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 7.4e+02;  
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 7 CTACGTTGACAGGAG 22  
 Db 16 CTCGCTGCACACGTAG 1  
 RESULT 696  
 ADB00356/C  
 ID ADB00356 standard; DNA; 17 BP.  
 XX AC ADB00356;  
 XX DT 20-NOV-2003 (first entry)  
 XX DE Human MD23 scanning oligonucleotide SEQ ID 1342.  
 XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 XX KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 XX KW developmental disorder; ss.  
 XX OS Homo sapiens.  
 XX PN EP1281758-A2.

PD 05-FEB-2003.  
 XX 30-JUL-2002; 2002EP-00016874.  
 XX  
 XX 02-AUG-2001; 2001US-00922181.  
 XX (AEOM-) AEOMICA INC.  
 PA Shannon M, Gu Y, Nguyen C;  
 PI WPI; 2003-423107/40.  
 XX  
 XX New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MDZ3,  
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
 XX  
 XX Example 8; SEQ ID NO 1342; 103pp; English.  
 PS  
 XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MDZ3,  
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 XX Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 22.9%; Score 6.4; DB 1; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 7.4e+02;  
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 4 GCCTACGCTGACAGG 19  
 Db 17 GCACTCGCTGCACACG 2  
 RESULT 697  
 ADB00357/c  
 ID ADB00357 standard; DNA; 17 BP.  
 XX  
 AC ADB00357;  
 XX 20-NOV-2003 (first entry)  
 DT Human MDZ3 scanning oligonucleotide SEQ ID 1343.  
 XX  
 DE Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX Homo sapiens.  
 OS  
 XX EP1281758-A2.  
 PN 05-FEB-2003.  
 XX 30-JUL-2002; 2002EP-00016874.  
 XX 02-AUG-2001; 2001US-00922181.  
 XX (AEOM-) AEOMICA INC.  
 PA Shannon M, Gu Y, Nguyen C;  
 PI WPI; 2003-423107/40.  
 XX  
 XX New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MDZ3,  
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
 XX  
 XX Example 8; SEQ ID NO 1342; 103pp; English.  
 PS  
 XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MDZ3,  
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 XX Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
 SQ

PI Shannon M, Gu Y, Nguyen C;  
 XX WPI; 2003-423107/40.  
 DR  
 XX New zinc finger-containing proteins and nucleic acids, useful in  
 XX manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MDZ3,  
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
 PT  
 XX Example 8; SEQ ID NO 1343; 103pp; English.  
 PS  
 XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MDZ3,  
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 XX Sequence 17 BP; 2 A; 4 C; 7 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 22.9%; Score 6.4; DB 1; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 7.4e+02;  
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 4 GCCTACGCTGACAGG 19  
 Db 16 GCACTCGCTGCACACG 1  
 RESULT 698  
 ADB01851/c  
 ID ADB01851 standard; DNA; 25 BP.  
 XX  
 AC ADB01851;  
 XX 20-NOV-2003 (first entry)  
 DT Human MDZ3 scanning oligonucleotide SEQ ID 2837.  
 XX  
 DE Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX Homo sapiens.  
 OS  
 XX EP1281758-A2.  
 PN 05-FEB-2003.  
 XX 30-JUL-2002; 2002EP-00016874.  
 XX 02-AUG-2001; 2001US-00922181.  
 XX (AEOM-) AEOMICA INC.  
 PA Shannon M, Gu Y, Nguyen C;  
 PI WPI; 2003-423107/40.  
 XX  
 XX New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MDZ3,  
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
 PT

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XX PS Example 8; SEQ ID NO 2837; 103pp; English.
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX CC or in manufacturing a medicament for treating or preventing a disorder
XX CC associated with decreased or increased expression or activity of MD23,
XX CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX CC acids can also be used as probes to detect and characterize gross
XX CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.
XX SQ Sequence 25 BP; 6 A; 6 C; 9 G; 4 T; 0 U; 0 Other;

Query Match      22.9%; Score 6.4; DB 1; Length 25;
Best Local Similarity 62.5%; Pred. No. 5.9e+02;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 CTACGCTGACAGGAG 22
Db 24 CTCGCTGCACAGTAG 9

RESULT 699
ADB01850/c
ID ADB01850 standard; DNA; 25 BP.
XX AC ADB01850;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD23 scanning oligonucleotide SEQ ID 2836.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX OS Homo sapiens.
XX FN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX FI Shannon M, Gu Y, Nguyen C;
XX DR WPI; 2003-423107/40.
XX PT New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MD23,
XX PT MD24, MD27 or MD212, e.g. cancer.
XX PS Example 8; SEQ ID NO 2836; 103pp; English.
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

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XX CC or in manufacturing a medicament for treating or preventing a disorder
XX CC associated with decreased or increased expression or activity of MD23,
XX CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX CC acids can also be used as probes to detect and characterize gross
XX CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.
XX SQ Sequence 25 BP; 7 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match      22.9%; Score 6.4; DB 1; Length 25;
Best Local Similarity 62.5%; Pred. No. 5.9e+02;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 CTACGCTGACAGGAG 22
Db 25 CTCGCTGCACAGTAG 10

RESULT 700
ABI00908
ID ABI00908 standard; DNA; 12 BP.
XX AC ABI00908;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 300881 for detecting SNP TSC0019231.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WC200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 300881; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

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Query Match	22.1%; Score 6.2; DB 1; Length 12;
Best Local Similarity	72.7%; Pred. No. 7e+02;
Matches	8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	7 CTACGCTGTACA 17 
Db	2 CTCCTCTTACA 12 
RESULT 701	
ABI54047	
ID	ABI54047 standard; DNA; 12 BP.
XX	AC
XX	AC
XX	ABI54047;
DT	22-FEB-2002 (first entry)
XX	
DE	Oligonucleotide primer SEQ ID NO 354020 for detecting SNP TSC0048852.
XX	
KW	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS	Homo sapiens.
XX	
XX	WO200117384-A2.
PN	
XX	18-OCT-2001.
PD	
XX	
XX	06-APR-2001; 2001WO-IB000713.
PF	
XX	07-APR-2000; 2000DE-01019173.
PR	
XX	(EPiG-) EPiGENOMICS AG.
PA	
XX	Olek A, Piepenbrock C, Berlin K;
PI	
XX	WPI; 2001-657177/75.
DR	
XX	
PT	Set of oligonucleotides, useful for diagnosis and cell typing, is
PT	designed to detect single-nucleotide polymorphisms and cytosine
PT	methylation status.
XX	
PS	Claim 1; SEQ ID NO 354020; 29pp + Sequence Listing; German.
XX	
CC	This invention describes novel oligonucleotide primers or peptide nucleic
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC	and cytosine methylation status in chemically pretreated genomic DNA. The
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC	range of diseases including immune system, gastrointestinal, respiratory,
CC	central nervous system, cardiovascular and metabolic disorders. The
CC	oligomers are also used for detecting cell type differentiation. ABC00010
CC	-ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC	represent the oligomers described in the invention. NOTE: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
Query Match	22.1%; Score 6.2; DB 1; Length 12;
Best Local Similarity	72.7%; Pred. No. 7e+02;
Matches	8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	7 CTACGCTGTACA 17 
Db	1 CTCCTCTTACA 11 
RESULT 702	
ABI21821	
ID	ABI21821 standard; DNA; 12 BP.
XX	

XX PD 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX DR WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 271278; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 3 A; 4 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 22.1%; Score 6.2; DB 1; Length 12;  
 Best Local Similarity 72.7%; Pred. No. 7e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 0;  
 QY 12 TGTACAGGAG 22  
 Db 12 TGTATACGAG 2  
 RESULT 704  
 ABI37455/C  
 ID ABI37455 standard; DNA; 12 BP.  
 AC ABI37455;  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide primer SEQ ID NO 337428 for detecting SNP TSC0039870.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 337428; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 3 A; 4 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 22.1%; Score 6.2; DB 1; Length 12;  
 Best Local Similarity 72.7%; Pred. No. 7e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 0;  
 QY 12 TGTACAGGAG 22  
 Db 12 TGTATACGAG 2

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 337428; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
 Query Match 22.1%; Score 6.2; DB 1; Length 12;  
 Best Local Similarity 72.7%; Pred. No. 7e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 CTACGTGTACA 17  
 Db 11 CTCCTTCTACA 1  
 RESULT 705  
 ABI72643  
 ID ABI72643 standard; DNA; 12 BP.  
 XX ABI72643;  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide primer SEQ ID NO 372616 for detecting SNP TSC0059501.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 372616; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
 SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 22.1%; Score 6.2; DB 1; Length 12;  
 Best Local Similarity 72.7%; Pred. No. 7e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 CTACGCTGAC 17  
 Db 2 CTCATATACA 12

RESULT 706  
 ABH72448/c  
 ID ABH72448 standard; DNA; 12 BP.  
 XX  
 AC ABH72448;  
 XX  
 XX 22-FEB-2002 (first entry)  
 DT  
 DE Oligonucleotide primer SEQ ID NO 272433 for detecting SNP TSC0002816.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 272433; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
 SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 22.1%; Score 6.2; DB 1; Length 12;  
 Best Local Similarity 72.7%; Pred. No. 7e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACGGGAG 22

Db 12 TGTATATGAG 2

RESULT 707  
 ABI22910/c  
 ID ABI22910 standard; DNA; 12 BP.  
 XX  
 AC ABI22910;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 322883 for detecting SNP TSC0031094.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 322883; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
 SQ Sequence 12 BP; 3 A; 0 C; 8 G; 1 T; 0 U; 0 Other;  
 Query Match 22.1%; Score 6.2; DB 1; Length 12;  
 Best Local Similarity 72.7%; Pred. No. 7e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CCTACGCTGAC 16  
 Db 12 CCTCCCTCTAC 2

RESULT 708  
 ABF18028  
 ID ABF18028 standard; DNA; 13 BP.  
 XX  
 AC ABF18028;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 118025 for detecting SNP TSC0029509.



XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
OS  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 118025; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
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SQ Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;  
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Query Match 22.1%; Score 6.2; DB 1; Length 13;  
Best Local Similarity 72.7%; Pred. No. 7.3e+02;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
Qy 12 TGTACAGGGAG 22  
Db 1 TGTAGAAGTAG 11  
XX  
RESULT 709  
ABF18029/c  
ID ABF18029 standard; DNA; 13 BP.  
XX  
AC ABF18029;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 118026 for detecting SNP TSC0029509.  
XX  
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
FN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX

PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 118026; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 22.1%; Score 6.2; DB 1; Length 13;  
Best Local Similarity 72.7%; Pred. No. 7.3e+02;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
Qy 12 TGTACAGGGAG 22  
Db 13 TGTAGAAGTAG 3  
XX  
RESULT 710  
ABC90236/c  
ID ABC90236 standard; DNA; 13 BP.  
XX  
AC ABC90236;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 90253 for detecting SNP TSC0022616.  
XX  
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 90253; 29pp + Sequence Listing; German.

```

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 22.1%; Score 6.2; DB 1; Length 13;
XX Best Local Similarity 72.7%; Pred. No. 7.3e+02;
XX Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 13 GTACAGGGAGT 23
XX      |||||
XX Db 12 GTACACGTATT 2
XX
XX RESULT 711
XX ID ABC90237 standard; DNA; 13 BP.
XX AC ABC90237;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 90254 for detecting SNP TSC0022616.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 90254; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 22.1%; Score 6.2; DB 1; Length 13;
XX Best Local Similarity 72.7%; Pred. No. 7.3e+02;
XX Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 13 GTACAGGGAGT 23
XX      |||||
XX Db 12 GTACACGTATT 2
XX
XX RESULT 712
XX ID ABF36729 standard; DNA; 13 BP.
XX AC ABF36729;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 136726 for detecting SNP TSC0034175.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 136726; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
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XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 22.1%; Score 6.2; DB 1; Length 13;
XX Best Local Similarity 72.7%; Pred. No. 7.3e+02;
XX Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 7 CTACGTGTACA 17
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XX Db 3 CTCACATTACA 13
XX
XX RESULT 713

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XX SQ Sequence 13 BP; 4 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
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XX Query Match 22.1%; Score 6.2; DB 1; Length 13;
XX Best Local Similarity 72.7%; Pred. No. 7.3e+02;
XX Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 13 GTACAGGGAGT 23
XX      |||||
XX Db 2 GTACACGTATT 12
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XX RESULT 712
XX ID ABF36729 standard; DNA; 13 BP.
XX AC ABF36729;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 136726 for detecting SNP TSC0034175.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
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XX PA (EPIG-) EPIGENOMICS AG.
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XX PI Olek A, Piepenbrock C, Berlin K;
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XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 136726; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
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XX SQ Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
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XX Query Match 22.1%; Score 6.2; DB 1; Length 13;
XX Best Local Similarity 72.7%; Pred. No. 7.3e+02;
XX Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 7 CTACGTGTACA 17
XX      |||||
XX Db 3 CTCACATTACA 13
XX
XX RESULT 713

```

ABF60519  
 ID ABF60519 standard; DNA; 13 BP.  
 AC ABF60519;  
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 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 160516 for detecting SNP TSC0040412.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 160516; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;  
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 CC Query Match 22.1%; Score 6.2; DB 1; Length 13;  
 CC Best Local Similarity 72.7%; Pred. No. 7.3e+02;  
 CC Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 QY 7 CTACGTGTACA 17  
 DB 1 CTCCTTCTACA 11  
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 RESULT 714  
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 ID ABF60516 standard; DNA; 13 BP.  
 XX  
 AC ABF60516;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 160513 for detecting SNP TSC0040412.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX

OS Homo sapiens.  
 XX  
 FN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 160513; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
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 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
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 CC ftp.wipo.int/pub/published\_pct\_sequences  
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 SQ Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
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 CC Best Local Similarity 72.7%; Pred. No. 7.3e+02;  
 CC Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 QY 7 CTACGTGTACA 17  
 DB 13 CTCCTTTTACA 3  
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 RESULT 715  
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 ID ABC56486 standard; DNA; 13 BP.  
 XX  
 AC ABC56486;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 56503 for detecting SNP TSC0015314.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 56503; 29pp + Sequence Listing; German.  
 XX  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
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 CC data for this patent did not form part of the printed specification, but  
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 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;  
 Query Match 22.1%; Score 6.2; DB 1; Length 13;  
 Best Local Similarity 72.7%; Pred. No. 7.3e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 13 GTACAGGGAGT 23  
 DB 2 GTAAACGTAGT 12  
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 RESULT 716  
 ABF82918  
 ID ABF82918 standard; DNA; 13 BP.  
 XX  
 AC ABF82918;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 182915 for detecting SNP TSC0045193.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 182915; 29pp + Sequence Listing; German.  
 XX  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;  
 Query Match 22.1%; Score 6.2; DB 1; Length 13;  
 Best Local Similarity 72.7%; Pred. No. 7.3e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 13 GTACAGGGAGT 23  
 DB 2 GTAAACGTAGT 12  
 ||| |||

CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;  
 Query Match 22.1%; Score 6.2; DB 1; Length 13;  
 Best Local Similarity 72.7%; Pred. No. 7.3e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 12 TGTACAGGGAG 22  
 DB 2 TGTATATGTAG 12  
 ||| |||  
 RESULT 717  
 ABF36728/c  
 ID ABF36728 standard; DNA; 13 BP.  
 XX  
 AC ABF36728;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 136725 for detecting SNP TSC0034175.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 136725; 29pp + Sequence Listing; German.  
 XX  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 22.1%; Score 6.2; DB 1; Length 13;  
 Best Local Similarity 72.7%; Pred. No. 7.3e+02;



XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 XX (EPIG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 120034; 29pp + Sequence Listing; German.  
 XX  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 13 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 22.1%; Score 6.2; DB 1; Length 13;  
 Best Local Similarity 72.7%; Pred. No. 7.3e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 12 TGTACAGGGAG 22  
 DB 12 TGTAAAAGTAG 2  
 RESULT 721  
 ABF60518/c  
 ID ABF60518 standard; DNA; 13 BP.  
 XX  
 XX ABF60518;  
 AC  
 XX 22-FEB-2002 (first entry)  
 DT  
 XX Oligonucleotide SEQ ID NO 160515 for detecting SNP TSC0040412.  
 DE  
 XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 PN  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 PR  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 160515; 29pp + Sequence Listing; German.  
 XX  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 22.1%; Score 6.2; DB 1; Length 13;  
 Best Local Similarity 72.7%; Pred. No. 7.3e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 CTACGTGTACA 17  
 DB 13 CTCCTTCTACA 3  
 RESULT 722  
 ABC56487/c  
 ID ABC56487 standard; DNA; 13 BP.  
 XX  
 XX ABC56487;  
 AC  
 XX 21-FEB-2002 (first entry)  
 DT  
 XX Oligonucleotide SEQ ID NO 56504 for detecting SNP TSC0015314.  
 DE  
 XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 PN  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 PR  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 56504; 29pp + Sequence Listing; German.  
 XX  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;  
 SQ

CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 22.1%; Score 6.2; DB 1; Length 13;  
 Best Local Similarity 72.7%; Pred. No. 7.3e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 13 GTACAGGGAGT 23  
 |||||  
 Db 12 GTAAAGTACT 2

## RESULT 723

ABF82919/c  
 ID ABF82919 standard; DNA; 13 BP.  
 AC ABF82919;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 182916 for detecting SNP TSC0045193.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 DF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX

PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PT  
 PS Claim 1; SEQ ID NO 182916; 29bp + Sequence Listing; German.  
 XX

CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 22.1%; Score 6.2; DB 1; Length 13;  
 Best Local Similarity 72.7%; Pred. No. 7.3e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 12 TGTACAGGGAG 22  
 |||||  
 Db 12 TGTATATGTAG 2

## RESULT 724

AAF46048  
 ID AAF46048 standard; DNA; 15 BP.  
 XX  
 AC AAF46048;  
 XX  
 DT 30-MAR-2001 (first entry)  
 XX  
 DE IGFBP2 oligonucleotide #887.  
 XX  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; viricide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
 KW IGF binding protein; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.

XX Homo sapiens.  
 OS  
 XX  
 FN WO200078341-A1.  
 XX

XX 28-DEC-2000.  
 PD  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.  
 XX

XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PA Wraight CJ, Werther GA, Edmondson SR;  
 XX  
 PI WPI; 2001-041421/05.  
 XX

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 PT  
 XX

XX Example 6; Page 39; 201pp; English.  
 PS  
 XX

CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 3 A; 8 C; 1 G; 3 T; 0 U; 0 Other;  
 SQ

Query Match 22.1%; Score 6.2; DB 1; Length 15;  
 Best Local Similarity 72.7%; Pred. No. 7.7e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CTACGTGTACA 17  
 |||||  
 Db 2 CTCCTGCACA 12

## RESULT 725

AAF46045

ID AAF46045 standard; DNA; 15 BP.  
 XX AC AAF46045;  
 XX AC  
 DT 30-MAR-2001 (first entry)  
 XX DE  
 DE DE IGFBP2 oligonucleotide #884.  
 XX DE  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX OS Homo sapiens.  
 XX OS WO200078341-A1.  
 XX PN  
 XX PD 28-DEC-2000.  
 XX PD  
 XX PF 21-JUN-2000; 2000WO-AU000693.  
 XX PF  
 XX PR 21-JUN-1999; 99US-0140345P.  
 XX PR  
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX PA  
 XX PI Wright CJ, Werther GA, Edmondson SR;  
 XX PI WPI; 2001-041421/05.  
 XX DR  
 XX XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX PS Example 6; Page 39; 201pp; English.  
 XX PS  
 XX CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX SQ Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 22.1%; Score 6.2; DB 1; Length 15;  
 Best Local Similarity 72.7%; Pred. No. 7.7e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 CTACGCTGAC 17  
 Db |||||  
 5 CTCCTGCACA 15  
 RESULT 726  
 AAF46046  
 ID AAF46046 standard; DNA; 15 BP.  
 XX AC  
 AC AAF46046;  
 XX DT 30-MAR-2001 (first entry)  
 XX DE IGFBP2 oligonucleotide #886.

DT 30-MAR-2001 (first entry)  
 XX DE  
 DE DE IGFBP2 oligonucleotide #885.  
 XX DE  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX OS Homo sapiens.  
 XX OS WO200078341-A1.  
 XX PN  
 XX PD 28-DEC-2000.  
 XX PD  
 XX PF 21-JUN-2000; 2000WO-AU000693.  
 XX PF  
 XX PR 21-JUN-1999; 99US-0140345P.  
 XX PR  
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX PA  
 XX PI Wright CJ, Werther GA, Edmondson SR;  
 XX PI WPI; 2001-041421/05.  
 XX DR  
 XX XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX PS Example 6; Page 39; 201pp; English.  
 XX PS  
 XX CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX SQ Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 22.1%; Score 6.2; DB 1; Length 15;  
 Best Local Similarity 72.7%; Pred. No. 7.7e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 CTACGCTGAC 17  
 Db |||||  
 4 CTCCTGCACA 14  
 RESULT 727  
 AAF46047  
 ID AAF46047 standard; DNA; 15 BP.  
 XX AC  
 AC AAF46047;  
 XX DT 30-MAR-2001 (first entry)  
 XX DE IGFBP2 oligonucleotide #886.



KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth factor 1 receptor; IGF-1; ptyriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW Growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX  
 XX 21-JUN-1999; 99US-0140345P.  
 XX  
 PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 XX Wright CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.  
 XX  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 XX Example 6; Page 39; 201pp; English.  
 XX  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 22.1%; Score 6.2; DB 1; Length 15;  
 Best Local Similarity 72.7%; Pred. No. 7.7e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 CTACGGTGACA 17  
 DB |||||  
 3 CTCCTGACACA 13  
 RESULT 728  
 AAT54219/C  
 ID AAT54219 standard; RNA; 15 BP.  
 AC AAT54219;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 24-MAR-1997 (first entry)  
 XX  
 XX Human IL-5 hammerhead ribozyme target sequence (nt. position 91).  
 DE  
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;

KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
 KW translocation; chronic myelogenous leukaemia; CML; cancer;  
 KW Philadelphia chromosome; inflammation; autoimmune disease;  
 KW atherosclerosis; myocardial infarction; stroke; restenosis;  
 KW transplant rejection; rheumatoid arthritis; psoriasis;  
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 XX  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9523225-A2.  
 XX  
 PD 31-AUG-1995.  
 XX  
 XX 23-FEB-1995; 95WO-IB000156.  
 XX  
 XX 23-FEB-1994; 94US-00201109.  
 PR 29-MAR-1994; 94US-00218934.  
 PR 04-APR-1994; 94US-00222795.  
 PR 07-APR-1994; 94US-00224483.  
 PR 15-APR-1994; 94US-00227958.  
 PR 15-APR-1994; 94US-00228041.  
 PR 18-MAY-1994; 94US-00245736.  
 PR 06-JUL-1994; 94US-00271280.  
 PR 15-AUG-1994; 94US-00291932.  
 PR 16-AUG-1994; 94US-00291433.  
 PR 17-AUG-1994; 94US-00292620.  
 PR 19-AUG-1994; 94US-00293520.  
 PR 02-SEP-1994; 94US-00300000.  
 PR 08-SEP-1994; 94US-00303039.  
 PR 23-SEP-1994; 94US-00311486.  
 PR 23-SEP-1994; 94US-00311749.  
 PR 28-SEP-1994; 94US-00314397.  
 PR 03-OCT-1994; 94US-00316771.  
 PR 11-OCT-1994; 94US-00319492.  
 PR 04-NOV-1994; 94US-00321993.  
 PR 10-NOV-1994; 94US-00337808.  
 PR 28-NOV-1994; 94US-00345516.  
 PR 16-DEC-1994; 94US-00357577.  
 PR 23-DEC-1994; 94US-00363233.  
 PR 30-JAN-1995; 95US-00380734.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;  
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;  
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Usman N, Wincott PE, Woolf T;  
 XX WPI; 1995-351090/45.  
 XX  
 XX Ribozymes having modified bases and methods for producing them - for use  
 PT in inhibiting disease related genes.  
 XX  
 XX Claim 2; Page 214; 407pp; English.  
 XX  
 XX The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-  
 CC 5) mRNA at the nucleotide base position indicated in the DE line. Regions  
 CC of the mRNA that do not form secondary folding structures and that  
 CC contain potential hammerhead and hairpin ribozyme cleavage sites were  
 CC identified by computer analysis. Ribozymes directed against these mRNA  
 CC sequences were designed and synthesised with modifications that improve  
 CC their nuclease resistance. The ribozymes cleave the IL-5 target sequences  
 CC and thereby inhibit IL-5 expression, making them useful for treating  
 CC chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes  
 CC and preventing the recruitment and activation of eosinophils. The  
 CC ribozymes can also be used to treat eosinophilia (related to parasitic  
 CC infection or with pulmonary infiltration) and L-tryptophan-associated  
 CC eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI  
 CC field.)

```
XX SQ Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 22.1%; Score 6.2; DB 1; Length 15;
Best Local Similarity 72.7%; Pred. No. 7.6e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGGAGTC 24
Dbb|||||
14 TACACGTAGGC 4

RESULT 729
ADB00349/c
ID ADB00349 standard; DNA; 17 BP.
XX AC ADB00349;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD23 scanning oligonucleotide SEQ ID 1335.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX PT WPI; 2003-423107/40.
XX PT New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MD23,
XX PT MD24, MD27 or MD212, e.g. cancer.
XX PS Example 8; SEQ ID NO 1335; 103pp; English.
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX CC or in manufacturing a medicament for treating or preventing a disorder
XX CC associated with decreased or increased expression or activity of MD23
XX CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX CC acids can also be used as probes to detect and characterize gross
XX CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.
XX SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 22.1%; Score 6.2; DB 1; Length 17;
Best Local Similarity 72.7%; Pred. No. 7.6e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGGAG 22
Dbb|||||
15 TGCACACGTAG 5
```

```
Db |||||
16 TGCACACGTAG 6

RESULT 730
ADB00350/c
ID ADB00350 standard; DNA; 17 BP.
XX AC ADB00350;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD23 scanning oligonucleotide SEQ ID 1336.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX PT WPI; 2003-423107/40.
XX PT New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MD23,
XX PT MD24, MD27 or MD212, e.g. cancer.
XX PS Example 8; SEQ ID NO 1336; 103pp; English.
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX CC or in manufacturing a medicament for treating or preventing a disorder
XX CC associated with decreased or increased expression or activity of MD23
XX CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX CC acids can also be used as probes to detect and characterize gross
XX CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.
XX SQ Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 22.1%; Score 6.2; DB 1; Length 17;
Best Local Similarity 72.7%; Pred. No. 7.6e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGGAG 22
Dbb|||||
15 TGCACACGTAG 5

RESULT 731
ADB00352/c
ID ADB00352 standard; DNA; 17 BP.
XX
```

AC ADB00352;  
 XX  
 DT 20-NOV-2003 (first entry)  
 DE  
 DE Human MD23 scanning oligonucleotide SEQ ID 1338.  
 XX  
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX EP1281758-A2.  
 PN  
 XX 05-FEB-2003.  
 PD  
 XX  
 XX 30-JUL-2002; 2002EP-00016874.  
 XX  
 XX 02-AUG-2001; 2001US-00922181.  
 XX  
 XX (AEOM-) AEOMICA INC.  
 XX  
 XX Shannon M, Gu Y, Nguyen C;  
 XX  
 XX WPI; 2003-423107/40.  
 DR  
 XX  
 XX New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 XX  
 XX Example 8; SEQ ID NO 1338; 103pp; English.  
 XX  
 XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 XX Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 22.1%; Score 6.2; DB 1; Length 17;  
 Best Local Similarity 72.7%; Pred. No. 7.6e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 12 TGTACAGGGAG 22  
 |||||  
 Db 13 TGCACACGTAG 3  
 RESULT 732  
 ADB00351/c  
 ID ADB00351 standard; DNA; 17 BP.  
 XX  
 XX ADB00351;  
 AC  
 XX 20-NOV-2003 (first entry)  
 DT  
 XX Human MD23 scanning oligonucleotide SEQ ID 1337.  
 DE  
 DE Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 KW developmental disorder; ss.

KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX EP1281758-A2.  
 PN  
 XX 05-FEB-2003.  
 PD  
 XX  
 XX 30-JUL-2002; 2002EP-00016874.  
 XX  
 XX 02-AUG-2001; 2001US-00922181.  
 XX  
 XX (AEOM-) AEOMICA INC.  
 XX  
 XX Shannon M, Gu Y, Nguyen C;  
 XX  
 XX WPI; 2003-423107/40.  
 DR  
 XX  
 XX New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 XX  
 XX Example 8; SEQ ID NO 1337; 103pp; English.  
 XX  
 XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 XX Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 22.1%; Score 6.2; DB 1; Length 17;  
 Best Local Similarity 72.7%; Pred. No. 7.6e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 12 TGTACAGGGAG 22  
 |||||  
 Db 14 TGCACACGTAG 4  
 RESULT 733  
 ADB00348/c  
 ID ADB00348 standard; DNA; 17 BP.  
 XX  
 XX ADB00348;  
 AC  
 XX 20-NOV-2003 (first entry)  
 DT  
 XX Human MD23 scanning oligonucleotide SEQ ID 1334.  
 DE  
 DE Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX EP1281758-A2.  
 PN  
 XX 05-FEB-2003.  
 PD

XX 30-JUL-2002; 2002EP-00016874.  
XX  
XX  
XX 02-AUG-2001; 2001US-00922181.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
XX Shannon M, Gu Y, Nguyen C;  
XX WPI; 2003-423107/40.  
XX  
XX New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MD23,  
PT MD24, MD27 or MD212, e.g. cancer.  
XX  
XX Example 8; SEQ ID NO 1334; 103pp; English.  
XX  
XX The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MD23.  
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
XX Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
SQ

Query Match 22.1%; Score 6.2; DB 1; Length 17;  
Best Local Similarity 72.7%; Pred. No. 7.6e+02;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGGAG 22  
DB 17 TGCACACGTAG 7  
RESULT 734  
ABQ72155  
ID ABQ72155 standard; DNA; 9 BP.  
XX  
XX AC ABQ72155;  
XX  
XX 28-AUG-2002 (first entry)  
XX  
XX Zinc finger protein related oligonucleotide target SEQ ID NO:2453.  
XX  
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200242459-A2.  
XX  
XX 30-MAY-2002.  
XX  
XX 20-NOV-2001; 2001WO-US043438.  
XX  
XX 20-NOV-2000; 2000US-00716637.  
XX  
XX (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
XX Liu Q;  
XX WPI; 2002-500284/53.  
XX  
XX

XX New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.  
XX  
XX Example 1; Page 62; 81pp; English.  
XX  
XX The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target subunit. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target subunit, selecting the F2 zinc finger such that it  
CC binds to the S2 target subunit, and selecting the F3 zinc finger such  
CC that it binds to the S3 target subunit, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target subunits  
CC having the nucleotide G in the 5'-most position of the subunit. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention  
XX  
XX Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;  
SQ

Query Match 21.4%; Score 6; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCC 7  
DB 3 GGGCCC 8  
RESULT 735  
ABQ72156  
ID ABQ72156 standard; DNA; 9 BP.  
XX  
XX AC ABQ72156;  
XX  
XX 28-AUG-2002 (first entry)  
XX  
XX Zinc finger protein related oligonucleotide target SEQ ID NO:2454.  
XX  
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200242459-A2.  
XX  
XX 30-MAY-2002.  
XX  
XX 20-NOV-2001; 2001WO-US043438.  
XX  
XX 20-NOV-2000; 2000US-00716637.  
XX  
XX (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
XX Liu Q;  
XX WPI; 2002-500284/53.  
XX  
XX New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.  
PT

XX Example 1; Page 62; 81pp; English.

PS The present invention describes a zinc finger protein (I) that binds to a

CC target site, comprising a first (F1), a second (F2), and a third (F3)

CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the

CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),

CC and a third (S3) target sub-site. Also described are: (i) a polypeptide

CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and

CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it

CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it

CC binds to the S2 target sub-site, and selecting the F3 zinc finger such

CC that it binds to the S3 target sub-site, thus designing (I) that binds to

CC a target site. (I) is useful for recognition of triplet target sub-sites

CC having the nucleotide G in the 5'-most position of the sub-site. (I) is

CC useful in studying gene function, and for human therapeutics and plant

CC engineering. (I), (II) or (III) is useful in therapeutic methods to

CC modulate the expression of a target region within a subject, in

CC diagnostic methods for sequence specific detection of target nucleic acid

CC in a sample, and in assays to determine the phenotype and function of

CC gene expression. (I) has improved affinity and specificity for their

CC target sequences, as well as enhanced biological activity. ABQ71213 to

CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc

CC finger peptides which are given in the exemplification of the present

CC invention

SQ Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 21.4%; Score 6; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCC 7

Db 3 GGGCCC 8

RESULT 736

ADA64482

ID ADA64482 standard; DNA; 9 BP.

XX AC ADA64482;

XX 20-NOV-2003 (first entry)

DE Zinc finger target sequence DNA #940.

ds; target sequence; zinc finger protein;

multi-finger zinc finger protein; improved affinity;

improved specificity; enhanced biological activity.

Synthetic.

US2003068675-A1.

10-APR-2003.

20-NOV-2001; 2001US-00990186.

24-MAR-1999; 99US-0126238P.

24-MAR-1999; 99US-0126239P.

30-JUL-1999; 99US-0146595P.

30-JUL-1999; 99US-0146615P.

23-MAR-2000; 2000US-00535008.

20-NOV-2000; 2000US-00716637.

(LIUQ/) LIU Q.

Liu Q;

WPI; 2003-567233/53.

20-NOV-2001; 2001US-00990186.

24-MAR-1999; 99US-0126238P.

24-MAR-1999; 99US-0126239P.

30-JUL-1999; 99US-0146595P.

30-JUL-1999; 99US-0146615P.

23-MAR-2000; 2000US-00535008.

20-NOV-2000; 2000US-00716637.

(LIUQ/) LIU Q.

Liu Q;

WPI; 2003-567233/53.

Designing zinc finger protein that has three zinc fingers from N-terminus

PT and C-terminus that bind to subsites in 3' to 5' direction, in a target

PT site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 27; 34pp; English.

PS The invention relates to a method of designing a zinc finger protein. The

CC method is useful for designing a zinc finger protein. The method provides

CC multi-finger zinc finger proteins with improved affinity and specificity

CC for their target sequences, as well as enhanced biological activity. The

CC present sequence represents a zinc finger protein DNA target sequence.

SQ Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 21.4%; Score 6; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCC 7

Db 3 GGGCCC 8

RESULT 737

ADA64483

ID ADA64483 standard; DNA; 9 BP.

XX AC ADA64483;

XX 20-NOV-2003 (first entry)

DE Zinc finger target sequence DNA #941.

ds; target sequence; zinc finger protein;

multi-finger zinc finger protein; improved affinity;

improved specificity; enhanced biological activity.

Synthetic.

US2003068675-A1.

10-APR-2003.

20-NOV-2001; 2001US-00990186.

24-MAR-1999; 99US-0126238P.

24-MAR-1999; 99US-0126239P.

30-JUL-1999; 99US-0146595P.

30-JUL-1999; 99US-0146615P.

23-MAR-2000; 2000US-00535008.

20-NOV-2000; 2000US-00716637.

(LIUQ/) LIU Q.

Liu Q;

WPI; 2003-567233/53.

Designing zinc finger protein that has three zinc fingers from N-terminus

and C-terminus that bind to subsites in 3' to 5' direction, in a target

site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 27; 34pp; English.

PS The invention relates to a method of designing a zinc finger protein. The

CC method is useful for designing a zinc finger protein. The method provides

CC multi-finger zinc finger proteins with improved affinity and specificity

CC for their target sequences, as well as enhanced biological activity. The

CC present sequence represents a zinc finger protein DNA target sequence.

SQ Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 21.4%; Score 6; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCC 7

Db 3 GGGCCC 8

RESULT 738

ADA64484

ID ADA64484 standard; DNA; 9 BP.

XX AC ADA64484;

XX 20-NOV-2003 (first entry)

DE Zinc finger target sequence DNA #942.

ds; target sequence; zinc finger protein;

multi-finger zinc finger protein; improved affinity;

improved specificity; enhanced biological activity.

Synthetic.

US2003068675-A1.

10-APR-2003.

20-NOV-2001; 2001US-00990186.

24-MAR-1999; 99US-0126238P.

24-MAR-1999; 99US-0126239P.

30-JUL-1999; 99US-0146595P.

30-JUL-1999; 99US-0146615P.

23-MAR-2000; 2000US-00535008.

20-NOV-2000; 2000US-00716637.

(LIUQ/) LIU Q.

Liu Q;

WPI; 2003-567233/53.

Designing zinc finger protein that has three zinc fingers from N-terminus

	Matches	6;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	2	GGGCCC	7							
Db	3	GGGCCC	8							

Search completed: April 19, 2004, 15:00:31  
Job time : 4 secs

GenCore version 5.1.6  
Copyright (C) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 15:45:29 ; Search time 0.001 Seconds  
(without alignments)  
202.496 Million cell updates/sec

Title: US-10-024-396-3-COPY

Perfect score: 28

Sequence: 1 cgggcctacgtgtacaggatccagg 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 211 seqs, 3616 residues

Total number of hits satisfying chosen parameters: 422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 213 summaries

Database: pmdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	71.4	20	1	PCT-US02-39183-19
C 2	20	71.4	20	1	PCT-US02-39183-20
C 3	20	71.4	20	1	US-10-024-396-19
C 4	20	71.4	20	1	US-10-024-396-20
C 5	18.6	66.4	25	1	US-09-922-181A-2841
C 6	18.6	66.4	25	1	US-09-922-181A-2842
C 7	18.2	65.0	25	1	US-09-922-181A-2839
C 8	18.2	65.0	25	1	US-09-922-181A-2840
C 9	17.8	63.6	25	1	US-09-922-181A-2837
C 10	17.8	63.6	25	1	US-09-922-181A-2838
C 11	17.8	63.6	25	1	US-09-956-584-315298
C 12	17.8	63.6	25	1	US-09-922-017-318766
C 13	17.6	62.9	25	1	US-09-922-181A-2843
C 14	17.6	62.9	25	1	US-09-954-427A-59195
C 15	17.2	61.4	25	1	US-10-719-900-248399
C 16	17.2	61.4	25	1	US-60-427-808-248399
C 17	16.8	60.0	25	1	US-09-922-181A-2836
C 18	16.8	60.0	25	1	US-09-922-181A-2844
C 19	16.6	59.3	25	1	US-09-954-427A-108187
C 20	16.6	59.3	25	1	US-09-954-427A-134734
C 21	16.6	59.3	25	1	US-09-956-584-2663
C 22	16.6	59.3	25	1	US-10-355-577-23855
C 23	16.6	59.3	25	1	US-10-355-577-23855
C 24	16.6	59.3	25	1	US-60-234-017-31888
C 25	16.6	59.3	25	1	US-60-353-987-23855
C 26	16.6	59.3	25	1	US-60-353-987-592056
C 27	14.4	51.4	17	1	US-09-922-181A-1335
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C 29	14.4	51.4	20	1	US-10-713-457-197
C 30	14.4	51.4	20	1	US-10-714-195-197
C 31	14.2	50.7	19	1	US-08-983-605-203
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15 1 US-10-310-188-22105 Sequence 22105, A
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## ALIGNMENTS

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RESULT 1
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; Sequence 19, Application PC/TUS0239183
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD3611 EXPRESSION
; FILE REFERENCE: RTSP-0453
; CURRENT APPLICATION NUMBER: PCT/US02/39183
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10/024,396
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-39183-19

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Query Match 71.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CGGGCCCTACGTGTACAGG 20
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Db 20 CGGGCCCTACGTGTACAGG 1

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RESULT 2
PCT-US02-39183-20/c
; Sequence 20, Application PC/TUS0239183
; GENERAL INFORMATION:

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; APPLICANT: Kenneth W. Dobie
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION
; FILE REFERENCE: RTSF-0453
; CURRENT APPLICATION NUMBER: PCT/US02/39183
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10/024,396
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-39183-20

Query Match      71.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 19, Application US/10024396
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION
; FILE REFERENCE: RTS-0339
; CURRENT APPLICATION NUMBER: US/10/024,396
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-396-19

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Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION
; FILE REFERENCE: RTS-0339
; CURRENT APPLICATION NUMBER: US/10/024,396
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 20
; LENGTH: 20
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-396-20

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Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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PCT-US02-39183-20

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Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-922-181A-2841
; Sequence 2841, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AN
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2841
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2841

Query Match      66.4%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3 GGCCCTACGTGTACAGGAGTCCAG 27
Db      1 GGCCCTACGTGTACAGGAGTCCAG 25

RESULT 6
US-09-922-181A-2842
; Sequence 2842, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AN
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2842
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2842

Query Match      66.4%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4 GGCCCTACGTGTACAGGAGTCCAGG 28
Db      1 GGCCCTACGTGTACAGGAGTCCAGG 25

RESULT 7
US-09-922-181A-2839
; Sequence 2839, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AN
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
```

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; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2839
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2839

Query Match      65.0%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTACAGGAGTCC 25
   |||||
Db 3 GGCCTACGTGTACAGGAGTCC 25

RESULT 8
US-09-922-181A-2840
; Sequence 2840, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: ACOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2840

Query Match      65.0%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTACAGGAGTCC 25
   |||||
Db 2 GGCCTACGTGTACAGGAGTCC 24

RESULT 9
US-09-922-181A-2837
; Sequence 2837, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: ACOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2837
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2837

Query Match      63.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTACAGGAGT 23
   |||||
Db 5 GGCCTACGTGTACAGGAGT 25

RESULT 10
US-09-922-181A-2838
; Sequence 2838, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: ACOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2838

Query Match      63.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTACAGGAGT 23
   |||||
Db 4 GGCCTACGTGTACAGGAGT 24

RESULT 11
US-09-956-584-315298
; Sequence 315298, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 315298
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-315298

Query Match      63.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCTACGTGTACAGGAGTC 24
   |||||
Db 3 GGCCTACGTGTACAGGAGTC 23

RESULT 12
US-60-234-017-318766
; Sequence 318766, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittman, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 318766
; LENGTH: 25
; TYPE: DNA
```

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; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AW123720
US-60-234-017-318766

Query Match      63.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCTACGTGTACAGGAGTC 24
   ||||| ||||| ||||| |||||
Db 3 GGCCTGTGTACAGGAGTC 23

RESULT 13
US-09-922-181A-2843
; Sequence 2843, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEOmica-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: AeoMica Sequence Listing Engine
; SEQ ID NO 2843
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2843

Query Match      62.9%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CCCTACGTGTACAGGAGTCAGG 28
   ||||| ||||| ||||| |||||
Db 1 CCCTACGTGTGACGAGTCGTGG 24

RESULT 14
US-09-954-427A-59195
; Sequence 59195, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT APPLICATION NUMBER: US/09/954,427A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 59195
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-59195

Query Match      62.9%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTACAGGAGTC 26
   ||||| ||||| ||||| |||||
Db 2 GTCCCCAAGTGTGACGAGTC 25

RESULT 15
US-10-719-900-248399
; Sequence 248399, Application US/10719900
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```
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 248399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-248399

Query Match      61.4%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGGAGTCAGG 28
   ||||| ||||| ||||| |||||
Db 3 CTCCTGTACAGGAGTCAGG 24

RESULT 16
US-60-427-808-248399
; Sequence 248399, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 248399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-248399

Query Match      61.4%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGGAGTCAGG 28
   ||||| ||||| ||||| |||||
Db 3 CTCCTGTACAGGAGTCAGG 24

RESULT 17
US-09-922-181A-2836
; Sequence 2836, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AN
; FILE REFERENCE: AEOmica-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: AeoMica Sequence Listing Engine
; SEQ ID NO 2836
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2836

Query Match      60.0%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 134734
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-134734

Query Match          59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels 0;

QY      3 GGCCTACGTGTACAGGAGTCC 25
        |||||
Db       2 GGCCCTACGTGTGCGAGAGTGC 24
        |||||

RESULT 21
US-09-956-584-2663
; Sequence 2663, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 2663
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-2663

Query Match          59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels 0;

QY      6 CCTACGTGTACAGGGAGTCCAGG 28
        |||||
Db       2 CCTAAGTCGACAGGGAGTCCGG 24
        |||||

RESULT 22
US-10-355-577-23855
; Sequence 23855, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 23855
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-355-577-23855

Query Match          59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels 0;

QY      6 CCTACGTGTACAGGGAGTCCAGG 28
        |||||
Db       3 CCCACGTGTACAGGGGGTTCCGG 25
        |||||

RESULT 23
US-10-355-577-592056/c

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/ Sequence 592056, Application US/10355577
/ GENERAL INFORMATION:
/ APPLICANT: Mittmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
/ FILE REFERENCE: 3121
/ CURRENT APPLICATION NUMBER: US/10/355,577
/ CURRENT FILING DATE: 2003-01-31
/ NUMBER OF SEQ ID NOS: 997516
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 592056
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-355-577-592056

Query Match          59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      6 CCTACGTGTACAGGGAGTCCAGG 28
Db      24 CCTACGTGTCTAGGGACACCAGG 2

RESULT 24
US-60-234-017-31888
/ Sequence 31888, Application US/60234017
/ GENERAL INFORMATION:
/ APPLICANT: Mittmann, M
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mus
/ FILE REFERENCE: 3115
/ CURRENT APPLICATION NUMBER: US/60/234,017
/ CURRENT FILING DATE: 2000-09-20
/ NUMBER OF SEQ ID NOS: 605887
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 31888
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: GenBank AV359510
US-60-234-017-31888

Query Match          59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      6 CCTACGTGTACAGGGAGTCCAGG 28
Db      2  CCTAGTCGACAGGGAGTCCCGG 24

RESULT 25
US-60-353-987-23855
/ Sequence 23855, Application US/60353987
/ GENERAL INFORMATION:
/ APPLICANT: Mittmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
/ FILE REFERENCE: 3121
/ CURRENT APPLICATION NUMBER: US/60/353,987
/ CURRENT FILING DATE: 2002-02-01
/ NUMBER OF SEQ ID NOS: 997516
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 23855
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-353-987-23855

Query Match          59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      6 CCTACGTGTACAGGGAGTCCAGG 28
Db      2  CCTAGTCGACAGGGAGTCCCGG 24

RESULT 26
US-60-353-987-592056/c
/ Sequence 592056, Application US/60353987
/ GENERAL INFORMATION:
/ APPLICANT: Mittmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
/ FILE REFERENCE: 3121
/ CURRENT APPLICATION NUMBER: US/60/353,987
/ CURRENT FILING DATE: 2002-02-01
/ NUMBER OF SEQ ID NOS: 997516
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 592056
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-353-987-592056

Query Match          59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      6 CCTACGTGTACAGGGAGTCCAGG 28
Db      3  CCCACGTGTACAGGGGTTCCGG 25

RESULT 27
US-09-922-181A-1335
/ Sequence 1335, Application US/09922181A
/ GENERAL INFORMATION:
/ APPLICANT: Gu, Yizhong
/ APPLICANT: Nguyen, Cung-Tuong
/ TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MDZ7 ANI
/ FILE REFERENCE: AEOICA-12
/ CURRENT APPLICATION NUMBER: US/09/922,181A
/ CURRENT FILING DATE: 2001-12-12
/ NUMBER OF SEQ ID NOS: 7046
/ SOFTWARE: Acomica Sequence Listing Engine
/ SEQ ID NO 1335
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-922-181A-1335

Query Match          51.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  GGCCTACGTGTACAG 18
Db      2  GGCCTACGTGTGCAG 17

RESULT 28
US-09-922-181A-1336
/ Sequence 1336, Application US/09922181A
/ GENERAL INFORMATION:
/ APPLICANT: Gu, Yizhong
/ APPLICANT: Nguyen, Cung-Tuong
/ TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MDZ7 ANI
/ FILE REFERENCE: AEOICA-12
/ CURRENT APPLICATION NUMBER: US/09/922,181A
/ CURRENT FILING DATE: 2001-12-12
/ NUMBER OF SEQ ID NOS: 7046
```

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/ SOFTWARE: Aeomica Sequence Listing Engine
/ SEQ ID NO 1336
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-922-18.A-1336

Query Match          51.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGCCCTACGTGTACAG 18
    |||||
Db 1 GGCCCTACGTGTCCAG 15

RESULT 29
PCT-US03-36777-197/c
/ Sequence 197, Application PC/TUS0336777
/ GENERAL INFORMATION:
/ APPLICANT: Genomic Health
/ APPLICANT: Vall d' Hebron University Hospital
/ APPLICANT: Baker, Joffre
/ APPLICANT: Cronin, Maureen
/ APPLICANT: Shak, Steve
/ APPLICANT: Baselga, Jose
/ TITLE OF INVENTION: GENE EXPRESSION PROFILING OF EGFR
/ FILE REFERENCE: 39740-0005
/ CURRENT APPLICATION NUMBER: PCT/US03/36777
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR FILING DATE: 2003-11-15
/ NUMBER OF SEQ ID NOS: 372
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 197
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: primer
PCT-US03-36777-197

Query Match          51.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCTACGTGTACAGGA 21
    |||||
Db 20 CCTACGGGTACAGGA 5

RESULT 30
US-10-713-457-197/c
/ Sequence 197, Application US/10713457
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Joffre
/ APPLICANT: Cronin, Maureen
/ APPLICANT: Shak, Steve
/ APPLICANT: Baselga, Jose
/ TITLE OF INVENTION: GENE EXPRESSION PROFILING OF EGFR
/ FILE REFERENCE: 39740-0005
/ CURRENT APPLICATION NUMBER: US/10713,457
/ PRIOR FILING DATE: 2003-11-13
/ PRIOR FILING DATE: 2003-11-15
/ NUMBER OF SEQ ID NOS: 372
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 197
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence

Query Match          51.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCTACGTGTACAGGA 21
    |||||
Db 20 CCTACGGGTACAGGA 5

RESULT 31
US-10-714-195-197/c
/ Sequence 197, Application US/10714195
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Joffre
/ APPLICANT: Cronin, Maureen
/ APPLICANT: Shak, Steve
/ APPLICANT: Baselga, Jose
/ TITLE OF INVENTION: GENE EXPRESSION PROFILING OF EGFR
/ FILE REFERENCE: 39740-0005
/ CURRENT APPLICATION NUMBER: US/10714,195
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR FILING DATE: 60/427090
/ NUMBER OF SEQ ID NOS: 372
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 197
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: primer
US-10-714-195-197

Query Match          51.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCTACGTGTACAGGA 21
    |||||
Db 20 CCTACGGGTACAGGA 5

RESULT 32
US-08-983-605-203/c
/ Sequence 203, Application US/08983605A
/ GENERAL INFORMATION:
/ APPLICANT: Roder, Marion
/ TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
/ TITLE OF INVENTION: Triticum Aestivum and Tribe Triticeae and the Use of
/ FILE REFERENCE: 2936.10400
/ CURRENT APPLICATION NUMBER: US/08/983,605A
/ CURRENT FILING DATE: 1998-05-01
/ EARLIER APPLICATION NUMBER: DE 195 25 284.5
/ EARLIER FILING DATE: 1995-06-28
/ NUMBER OF SEQ ID NOS: 466
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 203
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Triticum aestivum
US-08-983-605-203

Query Match          50.7%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCCTACGTGTACAGGAG 22
```

Db 19 GCCTTAGCGGTACAGGAG 1  
RESULT 33  
US-09-532-263-19  
; Sequence 19, Application US/09532263  
; GENERAL INFORMATION:  
; APPLICANT: Hilton, Douglas J.  
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/532,263  
; FILING DATE: 22-Apr-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/702,665  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Presser, Leopold  
; REGISTRATION NUMBER: 19,827  
; REFERENCE/DOCKET NUMBER: 10296  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 203 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-532-263-19  
Query Match 50.7%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 45;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 10 CGGTACAGGAGTCCAGG 28  
Db 3 CCTGTACTTGGAGTCCAGG 21  
RESULT 34  
US-09-532-263-19  
; Sequence 19, Application US/09532263  
; GENERAL INFORMATION:  
; APPLICANT: Hilton, Douglas J.  
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/853,105  
; FILING DATE: 10-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/702,665  
; FILING DATE: 20-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Presser, Leopold  
; REGISTRATION NUMBER: 19,827  
; REFERENCE/DOCKET NUMBER: 10296  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 203 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-853-105-19  
Query Match 50.7%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 45;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 10 CGGTACAGGAGTCCAGG 28  
Db 3 CCTGTACTTGGAGTCCAGG 21  
RESULT 35  
US-09-922-181A-1337  
; Sequence 1337, Application US/09922181A  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; APPLICANT: Nguyen, Cung-Tuong  
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 AN  
; FILE REFERENCE: AEONICA-12  
; CURRENT APPLICATION NUMBER: US/09/922,181A  
; CURRENT FILING DATE: 2001-12-12  
; NUMBER OF SEQ ID NOS: 7046  
; SOFTWARE: Aeonica Sequence Listing Engine  
; SEQ ID NO 1337  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-922-181A-1337  
Query Match 49.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 31;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 4 GCCTACGTGTACAGG 20  
Db 1 GCCTACGTGTACAGG 17  
RESULT 36  
US-09-922-181A-1338  
; Sequence 1338, Application US/09922181A  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; APPLICANT: Nguyen, Cung-Tuong  
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 AN

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; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1338
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1338

Query Match      49.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 31;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCTACGTGTACAGGGA 21
   |||||
Db 1 CCTACGTGTACAGGGA 17

RESULT 37
US-09-922-181A-1339
; Sequence 1339, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 AND
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1339
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1339

Query Match      49.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 31;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCTACGTGTACAGGAG 22
   |||||
Db 1 CCTACGTGTACAGGAG 17

RESULT 38
US-09-922-181A-1340
; Sequence 1340, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 AND
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1340
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1340

Query Match      49.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 31;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGGAGT 23
   |||||
Db 1 CTACGTGTACAGGAGT 17

; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1334
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1334

Query Match      47.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred.No. 36;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTACA 17
   |||||
Db 3 GGCCCTACGTGTGCA 17

RESULT 40
US-08-633-792-6/c
; Sequence 6, Application US/08633792
; GENERAL INFORMATION:
; APPLICANT: Barrett, Graham L
; TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,792
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PM/1870
; FILING DATE: 18-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516)742-4343
; TELEFAX: (516)742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA oligonucleotide"
```



US-08-633-792-6

Query Match 47.9%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 42;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 TGTACAGGAGTCCA 26  
|||  
Db 17 TGTACAGGAGTCCA 3

RESULT 41

US-09-075-717-6/c  
Sequence 6, Application US/09075717  
GENERAL INFORMATION:  
APPLICANT: Barrett, Graham L.  
TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE SURVIVAL  
TITLE OF INVENTION: AND AGENTS USEFUL FOR SAME  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/075,717  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/633,792  
FILING DATE: 01-JUL-1996  
APPLICATION NUMBER: AU PM/1870  
FILING DATE: 18-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 10062  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516)742-4343  
TELEFAX: (516)742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA oligonucleotide"

US-09-075-717-6

Query Match 47.9%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 42;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 TGTACAGGAGTCCA 26  
|||  
Db 17 TGTACAGGAGTCCA 3

RESULT 42

US-09-918-779-35/c  
Sequence 35, Application US/09918779  
GENERAL INFORMATION:  
APPLICANT: Taupier, Raymond  
APPLICANT: Padigar, Muralidhara

US-09-918-779-35

Query Match 47.9%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 42;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 TGTACAGGAGTCCA 26  
|||  
Db 17 TGTACAGGAGTCCA 3

RESULT 43

US-10-624-932-35/c  
Sequence 35, Application US/10624932  
GENERAL INFORMATION:  
APPLICANT: Taupier, Raymond  
APPLICANT: Padigar, Muralidhara  
APPLICANT: Rastelli, Luca  
APPLICANT: Spaderna, Steven

US-10-624-932-35

Query Match 47.9%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 54;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 TACAGGAGTCCAGG 28  
|||  
Db 17 TACAGGAGTCCAGG 3

RESULT 44

US-10-624-932-35/c  
Sequence 35, Application US/10624932  
GENERAL INFORMATION:  
APPLICANT: Taupier, Raymond  
APPLICANT: Padigar, Muralidhara  
APPLICANT: Rastelli, Luca  
APPLICANT: Spaderna, Steven

US-10-624-932-35



APPLICANT: Susan M. Freier  
APPLICANT: Kenneth W. Dobie  
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRE  
FILE REFERENCE: RTS-0365  
CURRENT APPLICATION NUMBER: US/10/159,856  
CURRENT FILING DATE: 2002-05-31  
NUMBER OF SEQ ID NOS: 134  
SEQ ID NO 105  
LENGTH: 20  
TYPE: DNA  
ORGANISM: H. sapiens  
FEATURE:  
US-10-159-856-105

Query Match 47.1%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 58;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCTACGTGTACAGGA 21  
||| |||||  
Db 2 GCGCATCGTGTACAGGA 19

RESULT 48  
US-09-922-181A-1341  
Sequence 1341, Application US/09922181A  
GENERAL INFORMATION:  
APPLICANT: Gu, Yizhong  
APPLICANT: Shannon, Mark  
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 AND  
FILE REFERENCE: AEOMICA-12  
CURRENT APPLICATION NUMBER: US/09/922,181A  
CURRENT FILING DATE: 2001-12-12  
NUMBER OF SEQ ID NOS: 7046  
SOFTWARE: Aeomica Sequence Listing Engine  
SEQ ID NO 1341  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-922-181A-1341

Query Match 45.7%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TAGGTGTACAGGAGT 23  
||| |||||  
Db 1 TAGGTGTACAGGAGT 16

RESULT 49  
US-10-310-188-68257  
Sequence 68257, Application US/10310188  
GENERAL INFORMATION:  
APPLICANT: RosettaGenomics  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE  
FILE REFERENCE: 47487  
CURRENT APPLICATION NUMBER: US/10/310,188  
CURRENT FILING DATE: 2002-12-19  
NUMBER OF SEQ ID NOS: 86841  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 68257  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-310-188-68257

Query Match 45.7%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 52;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGAGTCCAGG 28  
||| |||||  
Db 1 GAAAGGAGTCCAGG 16

RESULT 50  
US-10-316-954-1633  
Sequence 1633, Application US/10316954  
GENERAL INFORMATION:  
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Escherichia coli O157:H7, complete genome.  
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: US/10/316,954  
CURRENT FILING DATE: 2002-12-12  
NUMBER OF SEQ ID NOS: 5998  
SOFTWARE: Proprietary  
SEQ ID NO 1633  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Escherichia coli O157:H7, complete genome.  
FEATURE:  
LOCATION: (1432166)...(1432181)  
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 20  
US-10-316-954-1633

Query Match 44.3%; Score 12.4; DB 1; Length 16;  
Best Local Similarity 92.9%; Pred. No. 46;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAGG 28  
||| |||||  
Db 3 ACAGGAGTACAGG 16

RESULT 51  
US-10-316-954-3538/c  
Sequence 3538, Application US/10316954  
GENERAL INFORMATION:  
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Escherichia coli O157:H7, complete genome.  
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: US/10/316,954  
CURRENT FILING DATE: 2002-12-12  
NUMBER OF SEQ ID NOS: 5998  
SOFTWARE: Proprietary  
SEQ ID NO 3538  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Escherichia coli O157:H7, complete genome.  
FEATURE:  
LOCATION: (2694503)...(2694518)  
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 44  
US-10-316-954-3538

Query Match 44.3%; Score 12.4; DB 1; Length 16;  
Best Local Similarity 92.9%; Pred. No. 46;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAGG 28  
||| |||||  
Db 14 ACAGGAGTACAGG 1

RESULT 52  
US-09-922-181A-1333  
Sequence 1333, Application US/09922181A  
GENERAL INFORMATION:  
APPLICANT: Gu, Yizhong  
APPLICANT: Shannon, Mark  
APPLICANT: Nguyen, Cung-Tuong  
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 ANI  
FILE REFERENCE: AEOMICA-12  
CURRENT APPLICATION NUMBER: US/09/922,181A

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/ CURRENT FILING DATE: 2001-12-12
/ NUMBER OF SEQ ID NOS: 7046
/ SOFTWARE: Acomica Sequence Listing Engine
/ SEQ ID NO 1333
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-922-181A-1333

Query Match      44.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 53;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTAC 16
   |||||
Db 4 GGCCTACGTGTGC 17

RESULT 53
US-10-310-188-36260
/ Sequence 36260, Application US/10310188
/ GENERAL INFORMATION:
/ APPLICANT: RosettaGenomics
/ TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
/ FILE REFERENCE: 47487
/ CURRENT APPLICATION NUMBER: US/10/310,188
/ CURRENT FILING DATE: 2002-12-19
/ NUMBER OF SEQ ID NOS: 86841
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 36260
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-310-188-36260

Query Match      44.3%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 20
   |||||
Db 2 CTACGTGTACAGG 15

RESULT 54
US-09-356-067-30
/ Sequence 30, Application US/09356067
/ GENERAL INFORMATION:
/ APPLICANT: North, Michael
/ APPLICANT: Nishina, Patsy
/ APPLICANT: Naggart, Juergen
/ TITLE OF INVENTION: NOBEL-TRAUTH, KONRAD
/ TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
/ NUMBER OF SEQUENCES: 67
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Bozicevic & Reed, LLP
/ STREET: 285 Hamilton Avenue, Suite 200
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94301
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/356,067
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:

/ CURRENT FILING DATE: 2001-12-12
/ NUMBER OF SEQ ID NOS: 7046
/ SOFTWARE: Acomica Sequence Listing Engine
/ SEQ ID NO 1333
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-922-181A-1333

APPLICATION NUMBER: 09/032,365
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-2CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-356-067-30

Query Match      44.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 69;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAGG 28
   |||||
Db 6 ACAGGAGACCAGG 19

RESULT 55
US-10-184-372-23
/ Sequence 23, Application US/10184372
/ GENERAL INFORMATION:
/ APPLICANT: Bank, Rudolf A.
/ APPLICANT: Van der Slot, Annemarie J.
/ APPLICANT: Zuurmond, Anne-Marie
/ APPLICANT: Te Koppele, Johannes M.
/ TITLE OF INVENTION: Modification of collagenous materials and medical treatment, di
/ TITLE OF INVENTION: and monitoring of fibrotic conditions
/ FILE REFERENCE: P60187US00
/ CURRENT APPLICATION NUMBER: US/10/184,372
/ CURRENT FILING DATE: 2003-06-19
/ PRIOR APPLICATION NUMBER: US 09/450,209
/ PRIOR FILING DATE: 1999-11-29
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 23
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: primer
US-10-184-372-23

Query Match      44.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 69;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAGG 28
   |||||
Db 3 ACAGGAGTCCAGG 16

RESULT 56
US-09-882-945A-275
/ Sequence 275, Application US/09882945A
/ GENERAL INFORMATION:
/ APPLICANT: Lyamichev, Victor
/ APPLICANT: Allawi, Hatim
/ APPLICANT: Dong, Fang
/ APPLICANT: Neri, Bruce
/ APPLICANT: Vener, Tatiana
/ TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
/ FILE REFERENCE: FORS-04586
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; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-16907-32

Query Match      42.9%; Score 12; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGT 23
   |||
Db 1 CGGTACAGGAGT 14

RESULT 62
US-09-922-181A-1331
; Sequence 1331, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannan, Mark
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1331
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1331

Query Match      42.9%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGT 14
   |||
Db 6 GGCCCTACGTGT 17

RESULT 63
US-09-922-181A-1332
; Sequence 1332, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannan, Mark
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1332
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1332

Query Match      42.9%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGT 14
   |||
Db 5 GGCCCTACGTGT 16

RESULT 64
US-09-869-169-2
; Sequence 2, Application US/09869169
; GENERAL INFORMATION:
; APPLICANT: Paulussen, Aimee
; APPLICANT: Armstrong, Martin
; TITLE OF INVENTION: Genotyping Cytochrome Expression
; FILE REFERENCE: 51639/001
; CURRENT APPLICATION NUMBER: US/09/869,169
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: GB 9828619.8
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-869-169-2

Query Match      42.1%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 57;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGGAGTCCAG 27
   |||
Db 2 GTACAGGGAGCACAG 16

RESULT 65
US-09-869-169B-2
; Sequence 2, Application US/09869169B
; GENERAL INFORMATION:
; APPLICANT: Paulussen, Aimee
; APPLICANT: Armstrong, Martin
; TITLE OF INVENTION: Genotyping Cytochrome Expression
; FILE REFERENCE: 51639/001
; CURRENT APPLICATION NUMBER: US/09/869,169B
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: GB 9828619.8
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-869-169B-2

Query Match      42.1%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 57;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGGAGTCCAG 27
   |||
Db 2 GTACAGGGAGCACAG 16

RESULT 66
US-10-719-900-248399/c
; Sequence 248399, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Wei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 248399
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-248399

Query Match      42.1%; Score 11.8; DB 1; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 TACGTGTACAGGAG 22
Db      17 TCCCTGTACAGGAG 3

RESULT 67
US-60-427-808-248399/c
; Sequence 248399, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 248399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-248399

Query Match      42.1%; Score 11.8; DB 1; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 TACGTGTACAGGAG 22
Db      17 TCCCTGTACAGGAG 3

RESULT 68
US-09-553-362-122
; Sequence 122, Application US/09553362
; GENERAL INFORMATION:
; APPLICANT: Bradfield, Christopher A.
; APPLICANT: Gu, Yi Zhong
; APPLICANT: Hogenesch, John B.
; TITLE OF INVENTION: cDNAs and Proteins Involved in Hypoxia, Circadian and Orphan Sign
; FILE REFERENCE: WARF-0044 (P98022)
; CURRENT APPLICATION NUMBER: US/09/553,362
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: PCT/US98/25314
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/066,863
; PRIOR FILING DATE: 1997-11-28
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-553-362-122

Query Match      40.7%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 48;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCCTACGTGTAC 16
Db      1 GCCTACGTGTTC 13

RESULT 69
US-10-287-787-6950/c
; Sequence 6950, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 6950
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (946131)...(946146)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 761
US-10-287-787-6950

Query Match      40.7%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 56;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAGG 28
Db      14 CAGGGCGTCCAGG 2

RESULT 70
US-10-287-787-20271/c
; Sequence 20271, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 20271
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (3035688)...(3035702)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 2244
US-10-287-787-20271

Query Match      40.7%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 56;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAGG 28
Db      14 CAGGGCGTCCAGG 2

RESULT 71
US-09-590-522-1
; Sequence 1, Application US/09590522
; GENERAL INFORMATION:
; APPLICANT: Dale, Roderic M.K.
; APPLICANT: Arrow, Amy
; APPLICANT: Thompson, Terry
; TITLE OF INVENTION: Homeopathic Anti-Inflammatory
; FILE REFERENCE: OLIG-023
; CURRENT APPLICATION NUMBER: US/09/590,522
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-590-522-1

Query Match          40.7%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 66;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CQTGTACAGGGAG 22
      ||||| |||||
Db 1 CQTGTCCAGGGAG 13

RESULT 72
PCT-US02-25943-46322/c
; Sequence 46322, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 46322
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (4497630)...(4497646)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 49628
PCT-US02-25943-46322

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAG 27
      ||||| |||||
Db 13 ACAGGGGTGCCAG 1

RESULT 73
PCT-US02-25943-46323/c
; Sequence 46323, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 46323
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (4497630)...(4497646)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 49628
PCT-US02-25943-46323

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAG 27
      ||||| |||||
Db 13 ACAGGGGTGCCAG 1
```

```
RESULT 74
US-09-745-237A-643/c
; Sequence 643, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 643
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-643

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGGGAGT 23
      ||||| |||||
Db 15 GTGTACAGCGAGT 3

RESULT 75
US-09-745-237A-1045/c
; Sequence 1045, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1045
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1045

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGGGAGT 23
      ||||| |||||
Db 17 GTGTACAGCGAGT 5

RESULT 76
US-09-745-237A-1120/c
; Sequence 1120, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1120
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
```



```
US-09-745-237A-1120
Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGCGAGT 23
    |||||
Db 14 GTGTACAGCGAGT 2

RESULT 77
US-09-930-423-643/c
; Sequence 643, Application US/09930423
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 643
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-643

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGCGAGT 23
    |||||
Db 15 GTGTACAGCGAGT 3

RESULT 78
US-09-930-423-1045/c
; Sequence 1045, Application US/09930423
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1045
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1045

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGCGAGT 23
    |||||
Db 17 GTGTACAGCGAGT 5

RESULT 79
US-09-930-423-1120/c
; Sequence 1120, Application US/09930423
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
```

```
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1120
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1120

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGCGAGT 23
    |||||
Db 14 GTGTACAGCGAGT 2

RESULT 80
US-10-227-565-46322/c
; Sequence 46322, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 46322
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (4497630) ... (4497646)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 496;
US-10-227-565-46322

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAG 27
    |||||
Db 13 ACAGGAGTCCAG 1

RESULT 81
US-10-227-565-46323/c
; Sequence 46323, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 46323
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (4497630) ... (4497646)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 496;
US-10-227-565-46323

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
```

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAG 27  
| | | | |  
Db 13 ACAGGGTGTCCAG 1

## RESULT 82

US-10-310-188-68063  
; Sequence 68063, Application US/10310188  
; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE  
; FILE REFERENCE: 47487  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 188  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 68063  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-310-188-68063

Query Match 40.7%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 76;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGGAGTCCAG 28  
| | | | |  
Db 1 CAGGGATTCAG 13

## RESULT 83

US-10-310-188-77630  
; Sequence 77630, Application US/10310188  
; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE  
; FILE REFERENCE: 47487  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 188  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 77630  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-310-188-77630

Query Match 40.7%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 76;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 TACAGGGAGTCCA 26  
| | | | |  
Db 5 TACAGTGTGTTCA 17

## RESULT 84

US-10-367-832A-46322/c  
; Sequence 46322, Application US/10367832A  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
; FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333  
; CURRENT FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 64158  
; SOFTWARE: Proprietary  
; SEQ ID NO 46322

LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
; FEATURE:  
; LOCATION: (4497630)...(4497646)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 4962  
US-10-367-832A-46322

Query Match 40.7%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 76;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAG 27  
| | | | |  
Db 13 ACAGGGTGTCCAG 1

## RESULT 85

US-10-367-832A-46323/c  
; Sequence 46323, Application US/10367832A  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
; FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333  
; CURRENT FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 64158  
; SOFTWARE: Proprietary  
; SEQ ID NO 46323  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
; FEATURE:  
; LOCATION: (4497630)...(4497646)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 4962  
US-10-367-832A-46323

Query Match 40.7%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 76;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAG 27  
| | | | |  
Db 13 ACAGGGTGTCCAG 1

## RESULT 86

PCT-US02-40948-342/c  
; Sequence 342, Application PC/TUS0240948  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: JONES, Karen Anne  
; APPLICANT: VALDES, Ana  
; APPLICANT: TOWNLEY, David J.  
; APPLICANT: MANGION, Johnathan M.  
; APPLICANT: GALWEY, Nicolas  
; APPLICANT: BENNETT, Simon T.  
; APPLICANT: MCKAY, Ian J.  
; APPLICANT: SCHAFER, Alan  
; TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISMS ASSOCIATED WITH OSTEOPOROSIS  
; FILE REFERENCE: PV-0015 PCT  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR FILING DATE: 2002-11-04  
; NUMBER OF SEQ ID NOS: 400  
; SOFTWARE: PERL Program  
; SEQ ID NO 342  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY misc\_feature  
OTHER INFORMATION: Incyte ID No: NOT304 B Primer Sequence  
PCT-US02-40948-342

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 71;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGTCCA 26  
DB 16 GAGTCCAGGAGTCCA 1

RESULT 87  
PCT-US95-03316-23  
Sequence 23, Application PC/TUS9503316  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS GENE, SOMATIC MUTATIONS IN THE MTS  
TITLE OF INVENTION: GENE, AND METHODS FOR DIAGNOSIS, PROGNOSIS AND THERAPY OF  
TITLE OF INVENTION: CANCER DUE TO THE MTS GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,088  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,581  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Saxe, Stephen A.  
REGISTRATION NUMBER: 38,609  
REFERENCE/DOCKET NUMBER: 24884-109348-PCT-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4848  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
PCT-US95-03316-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 71;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGTGTACAGGAGTCC 25  
DB 1 CGTGTCCAGGAGGCC 16

RESULT 88  
PCT-US95-03537-23  
Sequence 23, Application PC/TUS9503537  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND  
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS  
TITLE OF INVENTION: GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Saxe, Stephen A.  
REGISTRATION NUMBER: 38,609  
REFERENCE/DOCKET NUMBER: 24884-109348-PCT-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4848  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
PCT-US95-03537-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;

Best Local Similarity 81.2%; Pred. No. 71;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25  
|||||  
DB 1 CGGTCCAGGAGCCC 16

RESULT 89

US-08-474-083-23  
; Sequence 23, Application US/08474083  
; GENERAL INFORMATION:  
; APPLICANT: Skolnick, Mark H.  
; APPLICANT: Cannon-Albright, Lisa A.  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: GEMLINE MUTATIONS IN THE MTS GENE AND  
; METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS  
; TITLE OF INVENTION: GENE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,083  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/03537  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION NUMBER: US 08/251,938  
; FILING DATE: 01-JUN-1994  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,087  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,086  
; FILING DATE: 14-APR-1994  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 08/214,582  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,369  
; FILING DATE: 14-APR-1994  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,086  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,086  
; FILING DATE: 14-APR-1994  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 08/214,582  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-109348-G  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-474-083-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 71;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25  
|||||  
DB 1 CGGTCCAGGAGCCC 16

RESULT 90

US-08-479-731-23  
; Sequence 23, Application US/08479731  
; GENERAL INFORMATION:  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,731  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/03316  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/251,938  
; FILING DATE: 01-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,087  
; FILING DATE: 18-MAR-1994  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,086  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,369  
; FILING DATE: 14-APR-1994  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 08/214,582  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-109348-F  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-479-731-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 71;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25  
Db 1 CGGTCCAGGAGCCC 16

RESULT 91  
US-08-481-063-23  
; Sequence 23, Application US/08481063  
; GENERAL INFORMATION:  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: SOMATIC MUTATIONS IN THE MTS GENE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/481,063  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/03316  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/251,938  
; FILING DATE: 01-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,087  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,086  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,369  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/214,582  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-109348-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; US-08-481-063-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 71;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25  
Db 1 CGGTCCAGGAGCCC 16

RESULT 92  
US-10-310-188-34900  
; Sequence 34900, Application US/10310188  
; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES  
; FILE REFERENCE: 47487  
; CURRENT APPLICATION NUMBER: US/10/310,188  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 34900  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-310-188-34900

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 71;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 GTACAGGAGTCCAGG 28  
Db 1 GTGAGGTAGTCCAGG 16

RESULT 93  
PCT-US02-16840-1766  
; Sequence 1766, Application PC/TUS0216840  
; GENERAL INFORMATION:  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve  
; TITLE OF INVENTION: RAS, HER2 and HIV  
; FILE REFERENCE: 400/046 (MBHB02-326)  
; CURRENT APPLICATION NUMBER: PCT/US02/16840  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: US 60/296,249  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/294,140  
; PRIOR FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 6810  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 1766  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
; PCT-US02-16840-1766

Query Match 40.0%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 82;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGGAG 22  
Db 1 CCACCAGUACAGGAG 16

RESULT 94  
PCT-US02-16840A-1766  
; Sequence 1766, Application PC/TUS0216840A  
; GENERAL INFORMATION:  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve  
; TITLE OF INVENTION: RAS, HER2 and HIV  
; FILE REFERENCE: 400/046 (MBHB02-326)

CURRENT APPLICATION NUMBER: PCT/US02/16840A  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: US 60/296,249  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/294,140  
; PRIOR FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 6810  
; SOFTWARE: Patent version 3.0  
; SEQ ID NO 1766  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
PCT-US02-16840A-1766

Query Match 40.0%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 82;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CTACGTGTACAGGAG 22  
| | | | | | | | | | | | | | | | | | | | |  
Db 1 CCACCAGUACAGGAG 16

RESULT 95  
US-09-546-745A-6677  
; Sequence 6577, Application US/09546745A  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: Zwick, Michael  
; APPLICANT: Pavco, Pam  
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules  
; FILE REFERENCE: 237/193  
; CURRENT APPLICATION NUMBER: US/09/546,745A  
; CURRENT FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 7043  
; SOFTWARE: Patent version 3.0  
; SEQ ID NO 6677  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-546-745A-6677

Query Match 40.0%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 62.5%; Pred. No. 82;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CTACGTGTACAGGAG 22  
| | | | | | | | | | | | | | | | | | | | |  
Db 1 CUACAUGUACAGGAG 16

RESULT 96  
US-09-818-875-2950/c  
; Sequence 2950, Application US/09818875  
; GENERAL INFORMATION:  
; APPLICANT: Kniesc, Eric B.  
; APPLICANT: Gampier, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/09/818,875  
; CURRENT FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27

; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; PRIOR FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 2950  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-818-875-2950

Query Match 40.0%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 82;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 ACGTGTACAGGAGTC 24  
| | | | | | | | | | | | | | | | | | | | |  
Db 17 ACTTGTCCAGGAGGC 2

## RESULT 97

US-09-818-875-2951  
; Sequence 2951, Application US/09818875  
; GENERAL INFORMATION:  
; APPLICANT: Kniesc, Eric B.  
; APPLICANT: Gampier, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/09/818,875  
; CURRENT FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; PRIOR FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 2951  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-818-875-2951

Query Match 40.0%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 82;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 ACGTGTACAGGAGTC 24  
| | | | | | | | | | | | | | | | | | | | |  
Db 1 ACTTGTCCAGGAGGC 16

RESULT 98  
US-09-922-181A-1343  
; Sequence 1343, Application US/09922181A  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannou, Mark  
; APPLICANT: Nguyen, Cung-Tuong  
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND  
; FILE REFERENCE: AEWICA-12  
; CURRENT APPLICATION NUMBER: US/09/922,181A  
; CURRENT FILING DATE: 2001-12-12  
; NUMBER OF SEQ ID NOS: 7046  
; SOFTWARE: AEWICA Sequence Listing Engine  
; SEQ ID NO 1343  
; LENGTH: 17

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1343

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTGACAGGAGTCC 25
Db 1 CGGTGACAGGAGTCC 16

RESULT 99
US-10-156-306-7026
; Sequence 7026, Application US/10156306
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156.306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7026
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-7026

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 82;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCAG 27
Db 2 UGCAGAGGGAGUACAG 17

RESULT 100
US-10-156-306-7027
; Sequence 7027, Application US/10156306
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156.306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7027
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-7027

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 82;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCAG 27
Db 1 UGCAGAGGGAGUACAG 16

RESULT 101
US-10-209-787-2950/c
; Sequence 2950, Application US/10209787
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-2951

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGAGTCC 24
Db 1 ACTTGTCCAGGAGGC 16

RESULT 102
US-10-209-787-2951
; Sequence 2951, Application US/10209787
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-2951

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGAGTCC 24
Db 1 ACTTGTCCAGGAGGC 16
```

```
RESULT 103
US-10-238-700-3087
; Sequence 2951, Application US/10261185
; GENERAL INFORMATION:
; APPLICANT: Kmlec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2951
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-238-700-3087

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGGAG 22
DB 1 CCACCAGUACAGGAG 16

RESULT 104
US-10-261-185-2950/c
; Sequence 2950, Application US/10261185
; GENERAL INFORMATION:
; APPLICANT: Kmlec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2950
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-2950

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGAGTC 24
DB 17 ACTGTCCAGGAGGC 2

RESULT 105
US-10-261-185-2951
; Sequence 2951, Application US/10261185
; GENERAL INFORMATION:
; APPLICANT: Kmlec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-2951

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGAGTC 24
DB 1 ACTGTCCAGGAGGC 16

RESULT 106
US-10-310-188-41474
; Sequence 41474, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 41474
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-41474

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCGCTACGTGTACAGG 19
DB 2 GCGCTACGATTACAGG 17

RESULT 107
US-10-310-188-74621/c
; Sequence 74621, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
```



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; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74621
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-74621

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 CCTACGTTGACAGGGA 21
      |||||
Db      16 CCTCGTGGCCAGGGA 1

RESULT 108
US-10-471-271-2304
; Sequence 2304, Application US/10471271
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Fosnaugh, Kathy
; TITLE OF INVENTION: Modulation of Gene Expression Associated with Inflammation Prolif
; TITLE OF INVENTION: and Neurite Growth Using Nucleic Acid Based Technologies
; FILE REFERENCE: MHBH 02-258-PCT (400/045)
; CURRENT APPLICATION NUMBER: US/10/471,271
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/294,412
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 13274
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2304
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-10-471-271-2305

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 82;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      12 TGTACAGGGAGTCCAG 27
      :|||
Db      1 UGCAGAGGGAGUACAG 16

RESULT 110
US-10-605-840-2080/c
; Sequence 2080, Application US/10605840
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VACCINIA REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55027
; CURRENT APPLICATION NUMBER: US/10/605,840
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 3750
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2080
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-840-2080

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      8 TACGTGTACAGGAGT 23
      |||||
Db      17 TACAAGTACAGTGAGT 2

RESULT 111
US-10-623-107-2950/c
; Sequence 2950, Application US/10623107
; GENERAL INFORMATION:
; APPLICANT: KMEC, ERIC B.
; TITLE OF INVENTION: TARGETED NUCLEIC ACID SEQUENCE ALTERATION USING PLURAL
; TITLE OF INVENTION: OLIGONUCLEOTIDES
; FILE REFERENCE: NAPRO-14 US
; CURRENT APPLICATION NUMBER: US/10/623,107
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/397,555
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: PatentIn ver 3.2
; SEQ ID NO 2950
```

```
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-623-107-2950

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGGAGTC 24
   |||||
Db 17 ACTTGTCAGGGAGGC 2

RESULT 112
US-10-623-107-2951
; Sequence 2951, Application US/10623107
; GENERAL INFORMATION:
; APPLICANT: KMEC, ERIC B.
; TITLE OF INVENTION: TARGETED NUCLEIC ACID SEQUENCE ALTERATION USING PLURAL
; FILE REFERENCE: NPRO-14 US
; CURRENT APPLICATION NUMBER: US/10/623,107
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/397,555
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: PatentIn ver 3.2
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-623-107-2951

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGGAGTC 24
   |||||
Db 17 ACTTGTCAGGGAGGC 16

RESULT 113
US-10-681-074-2950/c
; Sequence 2950, Application US/10681074
; GENERAL INFORMATION:
; APPLICANT: KMEC, ERIC B.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
; FILE REFERENCE: NPRO-18 US
; CURRENT APPLICATION NUMBER: US/10/681,074
; PRIOR FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US 60/453,360
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/416,983
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 4375
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2950
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-681-074-2950

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGGAGTC 24
   |||||
Db 17 ACTTGTCAGGGAGGC 2
```

```
RESULT 114
US-10-681-074-2951
; Sequence 2951, Application US/10681074
; GENERAL INFORMATION:
; APPLICANT: KMEC, ERIC B.
; APPLICANT: VAN BRABANT, ANJA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
; FILE REFERENCE: NPRO-18 US
; CURRENT APPLICATION NUMBER: US/10/681,074
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US 60/453,360
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/416,983
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 4375
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-681-074-2951
```

```
Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 9 ACGTGTACAGGGAGTC 24
   |||||
Db 1 ACTTGTCAGGGAGGC 16
```

```
RESULT 115
US-10-724-270-1766
; Sequence 1766, Application US/10724270
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: 400/046-US (MBH02-326-A)
; CURRENT APPLICATION NUMBER: US/10/724,270
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/US02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/238,700
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/157,580
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1766
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-724-270-1766
```

```
Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      7 CTACGTGTACAGGGAG 22
        ||| ||| ||| ||| |||
Db      1 CCACCAGUACAGGGAG 16
        ||| ||| ||| ||| |||

RESULT 116
US-60-339-764-2158/c
; Sequence 2158, Application US/60339764
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: AEOMICA-31
; CURRENT APPLICATION NUMBER: US/60/339,764
; NUMBER OF SEQ ID NOS: 3310
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2158
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-339-764-2158

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      13 GTACAGGAGTCCAGG 28
        ||| ||| ||| ||| |||
Db      17 GAAAGGAGTCAAGG 2
        ||| ||| ||| ||| |||

RESULT 117
US-60-339-764-2160/c
; Sequence 2160, Application US/60339764
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: AEOMICA-31
; CURRENT APPLICATION NUMBER: US/60/339,764
; NUMBER OF SEQ ID NOS: 3310
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2160
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-339-764-2160

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      12 TGTACAGGAGTCCAG 27
        ||| ||| ||| ||| |||
Db      16 TGAAGAGGAGTCAAG 1
        ||| ||| ||| ||| |||

RESULT 118
US-60-339-764-2303/c
; Sequence 2303, Application US/60339764
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: AEOMICA-31
; CURRENT APPLICATION NUMBER: US/60/339,764
; NUMBER OF SEQ ID NOS: 3310
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2303
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-339-764-2303

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 CCTACGTGTACAGGGA 21
        ||| ||| ||| ||| |||
Db      17 CCTACGTATAAGAGA 2
        ||| ||| ||| ||| |||

RESULT 119
US-60-339-764-2305/c
; Sequence 2305, Application US/60339764
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: AEOMICA-31
; CURRENT APPLICATION NUMBER: US/60/339,764
; NUMBER OF SEQ ID NOS: 3310
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2305
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-339-764-2305

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 CCTACGTGTACAGGG 20
        ||| ||| ||| ||| |||
Db      16 CCTACGTATAAGAG 1
        ||| ||| ||| ||| |||

RESULT 120
US-10-305-275-941/c
; Sequence 941, Application US/10305275
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Aeropyrum pernix K1 complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/305,275
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Proprietary
; SEQ ID NO 941
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Aeropyrum pernix K1 complete genome.
; FEATURE:
; LOCATION: (845005)...(845019)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectionObjectNumber = 13;
US-10-305-275-941

Query Match          39.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 GGGAGTCCAGG 28
        ||| ||| ||| ||| |||
Db      15 GGGAGTCCAGG 5
        ||| ||| ||| ||| |||

RESULT 121
US-10-305-275-942/c
; Sequence 942, Application US/10305275
```

```

; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Aeropyrum pernix K1 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/305,275
; CURRENT FILING DATE: 2002-11-28
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Proprietary
; SEQ ID NO 942
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Aeropyrum pernix K1 complete genome.
; FEATURE:
; LOCATION: (845005)...(845019)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1328
US-10-305-275-942

Query Match      39.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 GGGAGTCCAGG 28
      |||||
Db      15 GGGAGTCCAGG 5

RESULT 122
US-10-305-275A-941/c
; Sequence 941, Application US/10305275A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Aeropyrum pernix K1 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/305,275A
; CURRENT FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Proprietary
; SEQ ID NO 941
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Aeropyrum pernix K1 complete genome.
; FEATURE:
; LOCATION: (845005)...(845019)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1329
US-10-305-275A-941

Query Match      39.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 GGGAGTCCAGG 28
      |||||
Db      15 GGGAGTCCAGG 5

RESULT 123
US-10-305-275A-942/c
; Sequence 942, Application US/10305275A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Aeropyrum pernix K1 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/305,275A
; CURRENT FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Proprietary
; SEQ ID NO 942
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Aeropyrum pernix K1 complete genome.
; FEATURE:
; LOCATION: (845005)...(845019)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1328
US-10-305-275-942

Query Match      39.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 GGGAGTCCAGG 28
      |||||
Db      15 GGGAGTCCAGG 5

RESULT 124
US-10-310-188-56454
; Sequence 56454, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE OF INVENTION: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 56454
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-56454

Query Match      39.3%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 TGTACAGGGAG 22
      |||||
Db      6 TGTACAGGGAG 16

RESULT 125
PCT-US01-44838-5/c
; Sequence 5, Application PC/TUS0144838
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; TITLE OF INVENTION: Genetic Typing of Human Genes And Related Materials And Methods
; FILE REFERENCE: 4389-23-PCT
; CURRENT APPLICATION NUMBER: PCT/US01/44838
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 1449
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-44838-5

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      15 ACAGGGAGTCCAGG 28
      |||||
Db      15 ACAGGGTTCCAGG 2

RESULT 126
PCT-US02-25943-41393/c
; Sequence 41393, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
```

;/ CURRENT FILING DATE: 2002-08-27  
;/ NUMBER OF SEQ ID NOS: 64158  
;/ SOFTWARE: Proprietary  
;/ SEQ ID NO 41393  
;/ LENGTH: 15  
;/ TYPE: DNA  
;/ ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
;/ FEATURE:  
;/ LOCATION: (4017819)...(4017834)  
;/ OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 44331  
FCT-US02-25943-41393

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 71;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGAGTGCA 26  
Db 15 GCACAGGTAGTCCA 2

RESULT 127  
US-08-774-306-121  
;/ Sequence 121, Application US/08774306  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Draper, Kenneth G.  
;/ TITLE OF INVENTION: METHOD AND REAGENT FOR  
;/ TITLE OF INVENTION: INHIBITING HEPATITIS C  
;/ TITLE OF INVENTION: VIRUS REPLICATION  
;/ NUMBER OF SEQUENCES: 497  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Lyon & Lyon  
;/ STREET: 633 West Fifth Street  
;/ STREET: Suite 4700  
;/ CITY: Los Angeles  
;/ STATE: California  
;/ COUNTRY: U.S.A.  
;/ ZIP: 90071-2066

;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;/ MEDIUM TYPE: storage  
;/ COMPUTER: IBM Compatible  
;/ OPERATING SYSTEM: IBM P.C. DOS 5.0  
;/ SOFTWARE: Word Perfect 5.1  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/774,306  
;/ FILING DATE: 26-DEC-1996  
;/ CLASSIFICATION: 514  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/182,968  
;/ FILING DATE: 13-JANUARY-1994  
;/ APPLICATION NUMBER: 07/882,888  
;/ FILING DATE: 14-MAY-1992  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Warburg, Richard J.  
;/ REGISTRATION NUMBER: 32,327  
;/ REFERENCE/DOCKET NUMBER: 205/277  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (213) 489-1600  
;/ TELEFAX: (213) 955-0440  
;/ TELEX: 67-3510  
;/ INFORMATION FOR SEQ ID NO: 121:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 15  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear

US-08-774-306-121  
Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 71;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15  
Db 1 GGGCCCUCCGUGCA 14

RESULT 128  
US-09-274-553-678  
;/ Sequence 678, Application US/09274553A  
;/ GENERAL INFORMATION:  
;/ APPLICANT: RIBOZYNE PHARMACEUTICALS, INC.  
;/ APPLICANT: 2950 Wilderness Place  
;/ APPLICANT: Boulder, Colorado 80301  
;/ APPLICANT: USA  
;/ TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF  
;/ TITLE OF INVENTION: DISEASES OR CONDITIONS RELATED TO HEPATITIS C  
;/ TITLE OF INVENTION: VIRUS INFECTION  
;/ FILE REFERENCE: 241/078-FCT  
;/ CURRENT APPLICATION NUMBER: US/09/274,553A  
;/ CURRENT FILING DATE: 1999-03-23  
;/ PRIOR APPLICATION NUMBER: 09/274,553  
;/ PRIOR FILING DATE: 1999-03-23  
;/ PRIOR APPLICATION NUMBER: 09/257,608  
;/ PRIOR FILING DATE: 1999-02-25  
;/ PRIOR APPLICATION NUMBER: 60/100,842  
;/ PRIOR FILING DATE: 1998-09-18  
;/ PRIOR APPLICATION NUMBER: 60/083,217  
;/ PRIOR FILING DATE: 1998-04-27  
;/ NUMBER OF SEQ ID NOS: 3118  
;/ SOFTWARE: FastSeq for Windows Version 3.0  
;/ SEQ ID NO 678  
;/ LENGTH: 15  
;/ TYPE: RNA  
;/ ORGANISM: Hepatitis C Virus  
US-09-274-553-678

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 71;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15  
Db 1 GGGCCCUCCGUGCA 14

RESULT 129  
US-09-274-553B-143  
;/ Sequence 143, Application US/09274553B  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Blatt, Lawrence  
;/ APPLICANT: McSwiggen, James  
;/ APPLICANT: Roberts, Beth  
;/ APPLICANT: Pavco, Pamela  
;/ APPLICANT: Macejak, Dennis  
;/ TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT  
;/ TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
;/ FILE REFERENCE: IPI 247/282  
;/ CURRENT APPLICATION NUMBER: US/09/274,553B  
;/ CURRENT FILING DATE: 1999-03-23  
;/ PRIOR APPLICATION NUMBER: 09/257,608  
;/ PRIOR FILING DATE: 1999-02-24  
;/ PRIOR APPLICATION NUMBER: 60/100,842  
;/ PRIOR FILING DATE: 1998-09-18  
;/ PRIOR APPLICATION NUMBER: 60/083,217  
;/ PRIOR FILING DATE: 1998-04-27  
;/ NUMBER OF SEQ ID NOS: 3148  
;/ SOFTWARE: PatentIn version 3.0  
;/ SEQ ID NO 143  
;/ LENGTH: 15  
;/ TYPE: RNA  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-274-553B-143

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 71;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15  
|||||:|:|  
Db 1 GGGCCCUCCGUGCA 14

RESULT 130  
US-09-274-553C-143  
; Sequence 143, Application US/09274553C  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; FILE REFERENCE: tpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/274,553C  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3148  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 143  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-274-553C-143

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 71;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15  
|||||:|:|  
Db 1 GGGCCCUCCGUGCA 14

RESULT 131  
US-09-274-553D-143  
; Sequence 143, Application US/09274553D  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; FILE REFERENCE: tpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/274,553D  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3148  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 143  
; LENGTH: 15

TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-274-553D-143

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 71;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15  
|||||:|:|  
Db 1 GGGCCCUCCGUGCA 14

RESULT 132  
US-09-274-553E-143  
; Sequence 143, Application US/09274553E  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT  
; FILE REFERENCE: tpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/274,553E  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3148  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 143  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-274-553E-143

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 71;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15  
|||||:|:|  
Db 1 GGGCCCUCCGUGCA 14

RESULT 133  
US-09-504-231A-143  
; Sequence 143, Application US/09504231A  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT  
; FILE REFERENCE: tpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; PRIOR FILING DATE: 2000-02-15  
; CURRENT APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842

```
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-143

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGGCCCTACGTGTA 15
DB      1 GGGCCCUCCGUGCA 14

RESULT 134
US-09-504-231B-143
; Sequence 143, Application US/09504231B
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: MBH800-801-A (247/282)
; CURRENT APPLICATION NUMBER: US/09/504,231B
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; NUMBER OF SEQ ID NOS: 3258
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231B-143

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGGCCCTACGTGTA 15
DB      1 GGGCCCUCCGUGCA 14

RESULT 135
US-09-611-931-143
; Sequence 143, Application US/09611931
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
```

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; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: Ipi 250/285
; CURRENT APPLICATION NUMBER: US/09/611,931
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-611-931-143

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGGCCCTACGTGTA 15
DB      1 GGGCCCUCCGUGCA 14

RESULT 136
US-09-611-931A-143
; Sequence 143, Application US/09611931A
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: MBH800-801-B (250/285)
; CURRENT APPLICATION NUMBER: US/09/611,931A
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-09-611-931A-143

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGGCCCTACGTGTA 15
DB      1 GGGCCCUCCGUGCA 14

RESULT 137
US-09-633-515-121
; Sequence 121, Application US/09633515
```

GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 498  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: California  
ZIP: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/633,515  
FILING DATE: 2000-08-07  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/064,156  
FILING DATE: April 21, 1998  
APPLICATION NUMBER: 08/182,968  
FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882,888  
FILING DATE: May 14, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 234/083  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-633-515-121

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 71;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGA 15  
DB 1 GGGCCCTACGTGA 14

RESULT 138  
US-09-724-389-5/c  
; Sequence 5, Application US/09724389  
; GENERAL INFORMATION:  
; APPLICANT: Guida, Marco  
; APPLICANT: Hall, Jeff  
; TITLE OF INVENTION: Genetic Typing of Human Genes And Related Materials And Methods  
; FILE REFERENCE: 4389-23  
; CURRENT APPLICATION NUMBER: US/09/724,389  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 1449  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-389-5

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 71;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 15 ACAGGAGTCCAGG 28  
DB 15 ACAGGAGTCCAGG 2  
RESULT 139  
US-10-227-565-41393/c  
; Sequence 41393, Application US/10227565  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/227,565  
; CURRENT FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 64158  
; SOFTWARE: Proprietary  
; SEQ ID NO 41393  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
; FEATURE:  
; LOCATION: (4017819)...(4017834)  
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 443;  
US-10-227-565-41393

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 71;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 13 GTACAGGAGTCCCA 26  
DB 15 GCACAGGTAGTCCA 2

RESULT 140  
US-10-367-832A-41393/c  
; Sequence 41393, Application US/10367832A  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/367,832A  
; CURRENT FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 64158  
; SOFTWARE: Proprietary  
; SEQ ID NO 41393  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
; FEATURE:  
; LOCATION: (4017819)...(4017834)  
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 443;  
US-10-367-832A-41393

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 71;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 13 GTACAGGAGTCCCA 26  
DB 15 GCACAGGTAGTCCA 2

RESULT 141  
US-10-310-188-34441  
; Sequence 34441, Application US/10310188  
; GENERAL INFORMATION:  
; APPLICANT: Rosettacemomics  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES  
US-10-310-188-34441



Query Match	Best Local Similarity	Score	DB 1	Length 12	Indels	Mismatches	0	Gaps	0
Query Match	37.1%	Score 10.4;	DB 1;	Length 12;					
Best Local Similarity	91.7%	Pred. No. 47;							
Matches	11;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
<p>US-10-407-637-20</p> <p>LENGTH: 12</p> <p>TYPE: DNA</p> <p>ORGANISM: unknown</p> <p>FEATURE:</p> <p>OTHER INFORMATION: mutated pUC19</p>									
Query Match	37.1%	Score 10.4;	DB 1;	Length 12;					
Best Local Similarity	91.7%	Pred. No. 47;							
Matches	11;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
<p>US-10-407-637-20</p> <p>LENGTH: 12</p> <p>TYPE: DNA</p> <p>ORGANISM: unknown</p> <p>FEATURE:</p> <p>OTHER INFORMATION: mutated pUC19</p>									
Query Match	37.1%	Score 10.4;	DB 1;	Length 12;					
Best Local Similarity	91.7%	Pred. No. 47;							
Matches	11;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
<p>US-10-407-637-20</p> <p>LENGTH: 12</p> <p>TYPE: DNA</p> <p>ORGANISM: unknown</p> <p>FEATURE:</p> <p>OTHER INFORMATION: mutated pUC19</p>									
Query Match	37.1%	Score 10.4;	DB 1;	Length 12;					
Best Local Similarity	91.7%	Pred. No. 47;							
Matches	11;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
<p>US-10-407-637-20</p> <p>LENGTH: 12</p> <p>TYPE: DNA</p> <p>ORGANISM: unknown</p> <p>FEATURE:</p> <p>OTHER INFORMATION: mutated pUC19</p>									
Query Match	37.1%	Score 10.4;	DB 1;	Length 12;					
Best Local Similarity	91.7%	Pred. No. 47;							
Matches	11;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
<p>US-10-407-637-20</p> <p>LENGTH: 12</p> <p>TYPE: DNA</p> <p>ORGANISM: unknown</p> <p>FEATURE:</p> <p>OTHER INFORMATION: mutated pUC19</p>									
Query Match	37.1%	Score 10.4;	DB 1;	Length 12;					
Best Local Similarity	91.7%	Pred. No. 47;							
Matches	11;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
<p>US-10-407-637-20</p> <p>LENGTH: 12</p> <p>TYPE: DNA</p> <p>ORGANISM: unknown</p> <p>FEATURE:</p> <p>OTHER INFORMATION: mutated pUC19</p>									
Query Match	37.1%	Score 10.4;	DB 1;	Length 12;					
Best Local Similarity	91.7%	Pred. No. 47;							
Matches	11;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
<p>US-10-407-637-20</p> <p>LENGTH: 12</p> <p>TYPE: DNA</p> <p>ORGANISM: unknown</p> <p>FEATURE:</p> <p>OTHER INFORMATION: mutated pUC19</p>									
Query Match	37.1%	Score 10.4;	DB 1;	Length 12;					
Best Local Similarity	91.7%	Pred. No. 47;							
Matches	11;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
<p>US-10-407-637-20</p> <p>LENGTH: 12</p> <p>TYPE: DNA</p> <p>ORGANISM: unknown</p> <p>FEATURE:</p> <p>OTHER INFORMATION: mutated pUC19</p>									
Query Match	37.1%	Score 10.4;	DB 1;	Length 12;					
Best Local Similarity	91.7%	Pred. No. 47;							
Matches	11;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
<p>US-10-407-637-20</p> <p>LENGTH: 12</p> <p>TYPE: DNA</p> <p>ORGANISM: unknown</p> <p>FEATURE:</p> <p>OTHER INFORMATION: mutated pUC19</p>									
Query Match	37.1%	Score 10.4;	DB 1;	Length 12;					
Best Local Similarity	91.7%	Pred. No. 47;							
Matches	11;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
<p>US-10-407-637-20</p> <p>LENGTH: 12</p> <p>TYPE: DNA</p> <p>ORGANISM: unknown</p> <p>FEATURE:</p> <p>OTHER INFORMATION: mutated pUC19</p>									
Query Match	37.1%	Score 10.4;	DB 1;	Length 12;					
Best Local Similarity	91.7%	Pred. No. 47;							
Matches	11;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
<p>US-10-407-637-20</p> <p>LENGTH: 12</p> <p>TYPE: DNA</p> <p>ORGANISM: unknown</p> <p>FEATURE:</p> <p>OTHER INFORMATION: mutated pUC19</p>									
Query Match	37.1%	Score 10.4;	DB 1;	Length 12;					
Best Local Similarity	91.7%	Pred. No. 47;							
Matches	11;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
<p>US-10-407-637-20</p> <p>LENGTH: 12</p> <p>TYPE: DNA</p> <p>ORGANISM: unknown</p> <p>FEATURE:</p> <p>OTHER INFORMATION: mutated pUC19</p>									
Query Match	37.1%	Score 10.4;	DB 1;	Length 12;					

PCT-US01-26215-16

Query Match 37.1%; Score 10.4; DB 1; Length 15;  
Best Local Similarity 78.6%; Pred. No. 82;  
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 TACAGGAGTCCAG 27  
DB 2 TAAAGGAGTCCAG 15

RESULT 146

PCT-US01-26488-60  
; Sequence 60, Application PC/TUS0126488  
; GENERAL INFORMATION:  
; APPLICANT: Genaisance Pharmaceuticals, Inc.  
; APPLICANT: Anastasio, Alison E  
; APPLICANT: Chew, Anne  
; APPLICANT: Choi, Julie Y  
; APPLICANT: Kazemi, Amir  
; APPLICANT: Kliem, Stefanie E  
; APPLICANT: Koshiy, Beena  
; APPLICANT: Kumar, Anant Madan  
; APPLICANT: Parks, Katie E  
; TITLE OF INVENTION: HAPLOTYPES OF THE MTHFR GENE  
; FILE REFERENCE: MTHFR MHL077-PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/26488  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/227,757  
; PRIOR FILING DATE: 2000-08-24  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 60  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US01-26488-60

Query Match 37.1%; Score 10.4; DB 1; Length 15;  
Best Local Similarity 78.6%; Pred. No. 82;  
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGAC 16  
DB 2 GTCCCAACGTGTC 15

RESULT 147

PCT-US01-47434-7/c  
; Sequence 7, Application PC/TUS0147434  
; GENERAL INFORMATION:  
; APPLICANT: Genaisance Pharmaceuticals, Inc.  
; APPLICANT: Sanchis, Angela  
; APPLICANT: Sauser, Elizabeth Ann  
; APPLICANT: Shah, Nisha  
; TITLE OF INVENTION: HAPLOTYPES OF THE GPR6 GENE  
; FILE REFERENCE: GPR6 MWH-1648PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/47434  
; CURRENT FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/242,168  
; PRIOR FILING DATE: 2000-10-20  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US01-47434-7

Query Match 37.1%; Score 10.4; DB 1; Length 15;  
Best Local Similarity 91.7%; Pred. No. 82;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 AGGAGTCCAG 28  
DB 12 AGGAGTCCAG 1

RESULT 148

PCT-US02-25940-18950/c  
; Sequence 18950, Application PC/TUS0225940  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, plasmid  
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: PCT/US02/25940  
; CURRENT FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 25502  
; SOFTWARE: Proprietary  
; SEQ ID NO 18950  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Deinococcus radiodurans R1 complete genome, plasmid  
; FEATURE:  
; LOCATION: (2303965)...(2303980)  
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 2219  
PCT-US02-25940-18950

Query Match 37.1%; Score 10.4; DB 1; Length 15;  
Best Local Similarity 91.7%; Pred. No. 82;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27  
DB 13 CAGGAGTCCAG 2

RESULT 149

PCT-US02-25942-4864/c  
; Sequence 4864, Application PC/TUS0225942  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps  
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: PCT/US02/25942  
; CURRENT FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 15792  
; SOFTWARE: Proprietary  
; SEQ ID NO 4864  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps  
; FEATURE:  
; LOCATION: (1267742)...(1267757)  
; OTHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber = 507  
PCT-US02-25942-4864

Query Match 37.1%; Score 10.4; DB 1; Length 15;  
Best Local Similarity 91.7%; Pred. No. 82;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27  
DB 15 CAGGAGTCCAG 4

RESULT 150

PCT-US02-25942-6581/c  
; Sequence 6581, Application PC/TUS0225942  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps  
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: PCT/US02/25942  
; CURRENT FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 15792

```
; SOFTWARE: Proprietary
; SEQ ID NO 6581
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (3538785)...(3538798)
; OTHER INFORMATION: Chromosome = 3 Strand = negative ConnectronObjectNumber = 20087
PCT-US02-25942-6581

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
| | | | |
DB 15 CAGGAAGTCCAG 4

RESULT 151
PCT-US02-25943-22682/c
; Sequence 22682, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 22682
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2239343)...(2239357)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 24384
PCT-US02-25943-22682

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
| | | | |
DB 15 CAGGTAGTCCAG 4

RESULT 152
PCT-US02-25943-34828/c
; Sequence 34828, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 34828
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3391804)...(3391817)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 37318
PCT-US02-25943-34828

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
```

```
DB 15 CAGGTAGTCCAG 4

RESULT 153
PCT-US02-25943-37161/c
; Sequence 37161, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 37161
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3645015)...(3645029)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3983
PCT-US02-25943-37161

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
| | | | |
DB 15 CAGGTAGTCCAG 4

RESULT 154
PCT-US02-25943-48484
; Sequence 48484, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 48484
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (4677818)...(4677832)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 5192
PCT-US02-25943-48484

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
| | | | |
DB 3 CAGGAGTCCAG 14

RESULT 155
PCT-US02-25943-62741
; Sequence 62741, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
```

```
; SEQ ID NO 62741
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (6120631)...(6120645)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 67218
PCT-US02-25943-62741

Query Match      37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAG 27
      ||||| |||||
Db      3 CAGGGACTCCAG 14

RESULT 156
US-10-227-563-18950/c
; Sequence 18950, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 18950
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2303965)...(2303980)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 22195
US-10-227-563-18950

Query Match      37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAG 27
      ||||| |||||
Db      13 CAGGGCTCCAG 2

RESULT 157
US-10-227-565-22682/c
; Sequence 22682, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 22682
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2239343)...(2239357)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 24384
US-10-227-565-22682

Query Match      37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAG 27
      ||||| |||||
Db      15 CAGGGAGTCCAG 4

RESULT 158
US-10-227-565-34828/c
; Sequence 34828, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 34828
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3391804)...(3391817)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3731
US-10-227-565-34828

Query Match      37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAG 27
      ||||| |||||
Db      15 CAGGTAGTCCAG 4

RESULT 159
US-10-227-565-37161/c
; Sequence 37161, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 37161
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3645015)...(3645029)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3983
US-10-227-565-37161

Query Match      37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAG 27
      ||||| |||||
Db      15 CAGGTAGTCCAG 4

RESULT 160
US-10-227-565-48484
; Sequence 48484, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 48484
```

```
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (4677818)...(4677832)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 51923
US-10-227-565-48484
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
||| ||| ||| ||| |||
Db 3 CAGGGACTCCAG 14

RESULT 161
US-10-227-565-62741
; Sequence 62741, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 62741
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (6120631)...(6120645)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 67218
US-10-227-565-62741
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
||| ||| ||| ||| |||
Db 3 CAGGGACTCCAG 14

RESULT 162
US-10-227-567-4864/c
; Sequence 4864, Application US/10227567
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,567
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 4864
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (1267742)...(1267757)
; OTHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber = 5079
US-10-227-567-4864
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
||| ||| ||| ||| |||
Db 15 CAGGAAGTCCAG 4

RESULT 163
US-10-227-567-6581/c
; Sequence 6581, Application US/10227567
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,567
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 6581
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (3538785)...(3538798)
; OTHER INFORMATION: Chromosome = 3 Strand = negative ConnectronObjectNumber = 2001
US-10-227-567-6581
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
||| ||| ||| ||| |||
Db 15 CAGGAAGTCCAG 4

RESULT 164
US-10-287-787-27958/c
; Sequence 27958, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 27958
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (4016151)...(4016165)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 308
US-10-287-787-27958
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
||| ||| ||| ||| |||
Db 12 CAGGGCTCCAG 1

RESULT 165
US-10-367-729A-4864/c
; Sequence 4864, Application US/10367729A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,729A
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 4864
; LENGTH: 15
```

```

; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (1267742)...(1267757)
; OTHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber = 5075
US-10-367-729A-4864

Query Match      37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||| ||| ||| ||| |||
DB      15 CAGGAAGTCCAG 4

RESULT 166
US-10-367-729A-6581/c
; Sequence 6581, Application US/10367729A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,729A
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 6581
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (3538785)...(3538798)
; OTHER INFORMATION: Chromosome = 3 Strand = negative ConnectronObjectNumber = 20087
US-10-367-729A-6581

Query Match      37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||| ||| ||| ||| |||
DB      15 CAGGAAGTCCAG 4

RESULT 167
US-10-367-832A-22682/c
; Sequence 22682, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 22682
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2239343)...(2239357)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 24384
US-10-367-832A-22682

Query Match      37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||| ||| ||| ||| |||
DB      15 CAGGAGTCCAG 4

RESULT 168
US-10-367-832A-34828/c
; Sequence 34828, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 34828
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3391804)...(3391817)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 373
US-10-367-832A-34828

Query Match      37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||| ||| ||| ||| |||
DB      15 CAGGAGTCCAG 4

RESULT 169
US-10-367-832A-37161/c
; Sequence 37161, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 37161
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3645015)...(3645029)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 398
US-10-367-832A-37161

Query Match      37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||| ||| ||| ||| |||
DB      15 CAGGAGTCCAG 4

RESULT 170
US-10-367-832A-48484
; Sequence 48484, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 48484
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2239343)...(2239357)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 24384
US-10-367-832A-48484

Query Match      37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||| ||| ||| ||| |||
DB      15 CAGGAGTCCAG 4
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; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (4677818)...(4677832)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 51923
US-10-367-832A-48484
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
Db 3 CAGGGAGTCCAG 14

RESULT 171
US-10-367-832A-62741
; Sequence 62741, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 62741
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (6120631)...(6120645)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 67218
US-10-367-832A-62741
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
Db 3 CAGGGAGTCCAG 14

RESULT 172
US-10-367-892-18950/c
; Sequence 18950, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10367,892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 18950
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2303965)...(2303980)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 22195
US-10-367-892-18950
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
Db 13 CAGGGAGTCCAG 2

RESULT 173
PCT-US02-25943-33165/C
; Sequence 33165, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 33165
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3237918)...(3237933)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3554
PCT-US02-25943-33165
Query Match 37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
Db 16 CAGGTAGTCCAG 5

RESULT 174
PCT-US02-25943-33166
; Sequence 33166, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 33166
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3237919)...(3237934)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3555
PCT-US02-25943-33166
Query Match 37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
Db 2 CAGGTAGTCCAG 13

RESULT 175
PCT-US02-25943-34829
; Sequence 34829, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 34829
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.

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;
; FEATURE:
; LOCATION: (3391804)...(3391818)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 37320
PCT-US02-25943-34829

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAG 27
Db      2 CAGGTAGTCCAG 13

RESULT 176
US-10-227-565-33165/c
; Sequence 33165, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 33165
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3237918)...(3237933)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 35549
US-10-227-565-33165

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAG 27
Db      16 CAGGTAGTCCAG 5

RESULT 177
US-10-227-565-33166
; Sequence 33166, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 33166
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3237919)...(3237934)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 35550
US-10-227-565-33166

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAG 27
Db      2 CAGGTAGTCCAG 13

RESULT 178
US-10-227-565-34829
; Sequence 34829, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 34829
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3391804)...(3391818)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 37332
US-10-227-565-34829

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAG 27
Db      2 CAGGTAGTCCAG 13

RESULT 179
US-10-305-274-517
; Sequence 517, Application US/10305274
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Aquifex aeolicus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/305,274
; CURRENT FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 1550
; SOFTWARE: Proprietary
; SEQ ID NO 517
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Aquifex aeolicus complete genome.
; FEATURE:
; LOCATION: (532072)...(532087)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 7;
US-10-305-274-517

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 CGGTGTACAGGGA 21
Db      5 CGTTTACAGGGA 16

RESULT 180
US-10-305-274-1406
; Sequence 1406, Application US/10305274
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Aquifex aeolicus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/305,274
; CURRENT FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 1550
; SOFTWARE: Proprietary
; SEQ ID NO 1406
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Aquifex aeolicus complete genome.
; FEATURE:
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; LOCATION: (1394218)...(1394232)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1909
US-10-305-274-1406

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 CGGTACAGGGA 21
      ||| ||| ||| ||| |||
Db       5 CGTTACAGGGA 16

RESULT 181
US-10-367-832A-33165/c
; Sequence 33165, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 33165
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3237918)...(3237933)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 35549
US-10-367-832A-33165

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||| ||| ||| ||| |||
Db       16 CAGGTAGTCCAG 5

RESULT 182
US-10-367-832A-33166
; Sequence 33166, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 33166
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3237919)...(3237934)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 35550
US-10-367-832A-33166

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||| ||| ||| ||| |||
Db       2 CAGGTAGTCCAG 13

RESULT 183
US-10-367-832A-34829
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; Sequence 34829, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 34829
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3391804)...(3391818)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 373.
US-10-367-832A-34829

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||| ||| ||| ||| |||
Db       2 CAGGTAGTCCAG 13

RESULT 184
PCT-US02-25940-12401
; Sequence 12401, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 12401
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1491220)...(1491234)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 145(
PCT-US02-25940-12401

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      11 GTGTACAGGGAGTCC 25
      ||| ||| ||| ||| |||
Db       1 GCGTGCAGGGCGTCC 15

RESULT 185
PCT-US02-25940-14568
; Sequence 14568, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 14568
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1754821)...(1754835)
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; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 17012
PCT-US02-25940-14568

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGGGCCCTACGTGTA 15
   |||||
Db 1 CGGGCGGACGTGCA 15

RESULT 186
PCT-US02-25943-6183
; Sequence 6183, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 6183
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (542693)...(542707)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 6608
PCT-US02-25943-6183

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGGAGTCCAGG 28
   |||||
Db 1 TCGAGGGCGTGCAGG 15

RESULT 187
PCT-US02-25943-27773
; Sequence 27773, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 27773
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2698124)...(2698138)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 29757
PCT-US02-25943-27773

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGGAGTCCA 26
   |||||
Db 1 TGTAGAGGCGTCCA 15

RESULT 188
PCT-US02-25943-31162/c
; Sequence 31162, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31162
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3030196)...(3030210)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3336
PCT-US02-25943-31162

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGGGCCCTACGTGTA 15
   |||||
Db 15 CGGGCGCTTCGTGGA 1

RESULT 189
PCT-US02-25943-31163/c
; Sequence 31163, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31163
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3030196)...(3030210)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3336
PCT-US02-25943-31163

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGGGCCCTACGTGTA 15
   |||||
Db 15 CGGGCGCTTCGTGGA 1

RESULT 190
US-09-406-643-897/c
; Sequence 897, Application US/09406643
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Ludwig, Janos
; APPLICANT: Sproat, Brian
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
; FILE REFERENCE: MBH00-874-A (237/197)
; CURRENT APPLICATION NUMBER: US/09/406,643
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 08/879,078
; PRIOR FILING DATE: 1997-06-19
; PRIOR APPLICATION NUMBER: US 08/878,640
; PRIOR FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 897
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-406-643-897

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGGAGTCCAGG 28
DB 15 TCCTGGGAGCCAGG 1

RESULT 191
US-09-498-824A-897/c
; Sequence 897, Application US/09458824A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Ludwig, Janos
; APPLICANT: Spruat, Brian
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
; FILE REFERENCE: MEH00-874-D (247/280)
; CURRENT APPLICATION NUMBER: US/09/498,824A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 09/406,643
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 08/878,640
; PRIOR FILING DATE: 1997-06-19
; PRIOR APPLICATION NUMBER: US 08/879,078
; PRIOR FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 3516
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 897
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-498-824A-897

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGGAGTCCAGG 28
DB 15 TCCTGGGAGCCAGG 1

RESULT 192
US-09-611-577-21/c
; Sequence 21, Application US/09611577
; GENERAL INFORMATION:
; APPLICANT: Kazemi, Amir
; APPLICANT: Koshy, Beena
; APPLICANT: Duda, Amy
; APPLICANT: Genaisance Pharmaceuticals
; TITLE OF INVENTION: Drug Target Isogenes: Polymorphisms in the G
; FILE REFERENCE: MMH-567US
; CURRENT APPLICATION NUMBER: US/09/611,577
; CURRENT FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 21
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-611-577-21

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGGAGTCCAGG 28
DB 15 TCCTGGGAGCCAGG 1

RESULT 193
US-09-879-813-73/c
; Sequence 73, Application US/09879813
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005
; CURRENT APPLICATION NUMBER: US/09/879,813
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 73
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(110)
; OTHER INFORMATION: E264
; OTHER INFORMATION: The sequence ACA replaces the sequence GAGAG.46bp.CGTC
US-09-879-813-73

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCCTACGTGTACAG 18
DB 15 GCCCATGTGCACAG 1

RESULT 194
US-09-912-673A-55/c
; Sequence 55, Application US/09912673A
; GENERAL INFORMATION:
; APPLICANT: Ye, Bangce
; TITLE OF INVENTION: MEDIUM AND LOW DENSITY GENE CHIPS
; FILE REFERENCE: JNE 100
; CURRENT APPLICATION NUMBER: US/09/912,673A
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 55
; LENGTH: 15
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: P(qs)1 DNA probe
US-09-912-673A-55

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGGAGTC 24
DB 15 CTTGTCCAGGGAGGC 1

RESULT 195
US-09-912-673A-55
```

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US-10-146-505-73/c
; Sequence 73, Application US/10146505
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005B
; CURRENT APPLICATION NUMBER: US/10/146,505
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: GB 9822104.7
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: GB 9901141.3
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: GB 9913435.5
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(10)
; OTHER INFORMATION: F264
; OTHER INFORMATION: The sequence ACA replaces the sequence GAGAG.46bp.CGTG
US-10-146-505-73
Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCCTACGTGTACAG 18
    |||||
Db 15 GCCCATGTGCACAG 1

RESULT 196
US-10-227-563-12401
; Sequence 12401, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 12401
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1491220)...(1491234)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 14502
US-10-227-563-12401
Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GTGTACAGGAGTCC 25
    |||||
Db 1 GCGTGCAGGGGTCC 15

US-10-146-505-73/c
; Sequence 73, Application US/10146505
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005B
; CURRENT APPLICATION NUMBER: US/10/146,505
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: GB 9822104.7
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: GB 9901141.3
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: GB 9913435.5
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(10)
; OTHER INFORMATION: F264
; OTHER INFORMATION: The sequence ACA replaces the sequence GAGAG.46bp.CGTG
US-10-146-505-73
Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCCTACGTGTACAG 18
    |||||
Db 15 GCCCATGTGCACAG 1

RESULT 196
US-10-227-563-12401
; Sequence 12401, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 12401
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1491220)...(1491234)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 14502
US-10-227-563-12401
Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GTGTACAGGAGTCC 25
    |||||
Db 1 GCGTGCAGGGGTCC 15

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RESULT 197
US-10-227-563-14568
; Sequence 14568, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 14568
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1754821)...(1754835)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1701
US-10-227-563-14568
Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGGGCCCTACGTGTA 15
    |||||
Db 1 CGGGCGCGACGTGCA 15

RESULT 198
US-10-227-565-6183
; Sequence 6183, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 6183
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (542693)...(542707)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 66(
US-10-227-565-6183
Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 TACAGGAGTCCAGG 28
    |||||
Db 1 TGCAGGGCGTGCAGG 15

RESULT 199
US-10-227-565-27773
; Sequence 27773, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 27773
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.

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; FEATURE:
; LOCATION: (2698124)...(2698138)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 29757
US-10-227-565-27773
Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 12 TGTACAGGGAGTCCCA 26
Db 1 TGTACAGGGAGTCCCA 15
RESULT 200
US-10-227-565-31162/c
; Sequence 31162, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31162
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3030196)...(3030210)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 33368
US-10-227-565-31162
Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CGGGCCCTACGTGTA 15
Db 15 CGGGCGCTTCGTGGA 1
RESULT 201
US-10-227-565-31163/c
; Sequence 31163, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31163
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3030196)...(3030210)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 33365
US-10-227-565-31163
Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CGGGCCCTACGTGTA 15
Db 15 CGGGCGCTTCGTGGA 1
RESULT 202
US-10-227-565-31164/c
; Sequence 31164, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31164
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3030196)...(3030210)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 33366
US-10-227-565-31164
Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CGGGCCCTACGTGTA 15
Db 15 CGGGCGCTTCGTGGA 1
RESULT 203
US-10-287-787-16397/c
; Sequence 16397, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 16397
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (2480655)...(2480669)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 181
US-10-287-787-16397
Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 13 GTACAGGGAGTCCAG 27
Db 1 GTTACAGGAGGCCAG 15
RESULT 204
US-10-287-787-25557/c
; Sequence 25557, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 25557
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
```

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; LOCATION: (3679402)...(3679417)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 28230
US-10-287-787-25557

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 GTACAGGAGTCCAG 27
Db 15 GTTCAGGAGGCCAG 1

RESULT 205
US-10-310-188-22102
; Sequence 22102, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22102
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-22102

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCA 26
Db 1 TGTCCAGGCTGTCCA 15

RESULT 206
US-10-310-188-22105
; Sequence 22105, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22105
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-22105

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCA 26
Db 1 TGTCCAGGTTGTCCA 15

RESULT 207
US-10-367-832A-6183
; Sequence 6183, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 6183
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
US-10-367-832A-6183

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGGAGTCCAG 28
Db 1 TGCAGGGCGTGCAG 15

RESULT 208
US-10-367-832A-27773
; Sequence 27773, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 27773
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
US-10-367-832A-27773

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCA 26
Db 1 TGTAGAGGCGTCCA 15

RESULT 209
US-10-367-832A-31162/c
; Sequence 31162, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31162
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
US-10-367-832A-31162

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCA 26
Db 1 TGTCCAGGTTGTCCA 15

RESULT 207
US-10-367-832A-6183
; Sequence 6183, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 6183
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
US-10-367-832A-6183

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGGAGTCCAG 28
Db 1 TGCAGGGCGTGCAG 15

RESULT 208
US-10-367-832A-27773
; Sequence 27773, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 27773
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
US-10-367-832A-27773

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCA 26
Db 1 TGTAGAGGCGTCCA 15

RESULT 209
US-10-367-832A-31162/c
; Sequence 31162, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31162
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
US-10-367-832A-31162

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCA 26
Db 1 TGTCCAGGTTGTCCA 15

RESULT 207
US-10-367-832A-6183
; Sequence 6183, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 6183
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
US-10-367-832A-6183

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGGAGTCCAG 28
Db 1 TGCAGGGCGTGCAG 15

RESULT 208
US-10-367-832A-27773
; Sequence 27773, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 27773
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
US-10-367-832A-27773

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCA 26
Db 1 TGTAGAGGCGTCCA 15

RESULT 209
US-10-367-832A-31162/c
; Sequence 31162, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31162
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
US-10-367-832A-31162

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCA 26
Db 1 TGTCCAGGTTGTCCA 15

RESULT 207
US-10-367-832A-6183
; Sequence 6183, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 6183
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
US-10-367-832A-6183

Query Match 36.4%;
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Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGGGCCCTACGTGTA 15
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Db 15 CGGGCGCTTCGTGGA 1

RESULT 210
US-10-367-832A-31163/c
; Sequence 31163, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31163
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3030196)...(3030210)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 33365
US-10-367-832A-31163

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGGGCCCTACGTGTA 15
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Db 15 CGGGCGCTTCGTGGA 1

RESULT 211
US-10-367-892-12401
; Sequence 12401, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 12401
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1491220)...(1491234)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 14502
US-10-367-892-12401

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGTCC 25
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Db 1 CGGTGACAGGCGTCC 15

RESULT 212
US-10-367-892-14568
; Sequence 14568, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
US-10-367-892-14568

Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGGGCCCTACGTGTA 15
    ||||| |||||
Db 15 CGGGCGCTTCGTGGA 1

RESULT 213
US-10-453-850-897/c
; Sequence 897, Application US/10453850
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Ludwig, Janos
; APPLICANT: Sproat, Brian
; TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
; FILE REFERENCE: MBH00-874-A (237/197)
; CURRENT APPLICATION NUMBER: US/10/453,850
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: US/09/406,643
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 08/879,078
; PRIOR FILING DATE: 1997-06-19
; PRIOR APPLICATION NUMBER: US 08/878,640
; PRIOR FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 897
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-453-850-897

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGAGTCCAGG 28
    ||||| |||||
Db 15 TCCTGGGAGCCAGG 1

Search completed: April 19, 2004, 15:45:30
Job time : 1 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 15:06:48 ; Search time 0.001 Seconds  
(without alignments)  
116.984 Million cell updates/sec

Title: US-10-024-396-3-COPY  
Perfect score: 28  
Sequence: 1 cggccctacgtacagggagtcacagg 28

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 180 seqs, 2089 residues  
Total number of hits satisfying chosen parameters: 360

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 218 summaries

Database : issdb: \* *Issued - Patents - NA*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.2	50.7	21	1	US-08-702-665A-19
2	13.4	47.9	18	1	US-08-633-792A-6
3	13.4	47.9	18	1	US-09-075-717A-6
4	12.4	44.3	19	1	US-08-630-592-18
5	12.4	44.3	19	1	US-08-714-991-18
6	12.4	44.3	19	1	US-09-032-365A-30
7	12.2	43.6	18	1	US-08-117-952-129
8	12.2	43.6	18	1	US-08-970-269A-6
9	12.2	43.6	18	1	US-08-474-177-23
10	11.2	40.0	16	1	US-08-487-033-23
11	11.2	40.0	16	1	US-08-480-810-23
12	11.2	40.0	16	1	US-08-508-735-23
13	11.2	40.0	16	1	US-08-848-251-23
14	11.2	40.0	16	1	US-08-486-047-23
15	11.2	40.0	16	1	US-09-120-130-23
16	11.2	40.0	16	1	US-09-115-252-23
17	11.2	40.0	16	1	US-08-988-515-23
18	11.2	40.0	16	1	US-09-120-138-23
19	11.2	40.0	16	1	US-09-120-139-23
20	11.2	40.0	16	1	US-09-201-139-23
21	11.2	40.0	16	1	US-09-120-131-23
22	11.2	40.0	16	1	US-08-182-968A-121
23	10.8	38.6	15	1	US-08-774-306A-121
24	10.8	38.6	15	1	US-09-064-156A-121
25	10.8	38.6	15	1	US-09-081-646-121
26	10.8	38.6	15	1	US-09-180-437-185
27	10.4	37.1	15	1	US-08-182-968A-297
28	10	35.7	15	1	US-08-319-492B-24
29	10	35.7	15	1	US-08-774-306A-297
30	10	35.7	15	1	US-09-064-156A-297
31	10	35.7	15	1	US-09-698-505A-38
32	9.8	35.0	15	1	US-08-182-968A-115
33	9.8	35.0	15	1	US-08-182-968A-115

34	9.8	35.0	15	1	US-08-774-306A-115
35	9.8	35.0	15	1	US-09-064-156A-115
36	9.8	35.0	15	1	US-09-180-437-134
37	9.8	35.0	15	1	PCT-US93-02612-2
38	9.4	33.6	12	1	US-09-203-231B-67
39	9.4	33.6	12	1	5174962-2
40	9.4	33.6	12	1	5174962-2
41	9.2	32.9	14	1	US-08-623-891-20
42	9.2	32.9	14	1	US-09-340-861-20
43	9.2	32.9	14	1	US-09-634-262-20
44	9	32.1	12	1	US-08-494-301A-6
45	8.8	31.4	12	1	US-09-203-231B-67
46	8.8	31.4	12	1	US-09-281-418-211
47	8.8	31.4	13	1	US-09-014-304-3
48	8.8	31.4	13	1	US-09-874-601-30
49	8.4	30.0	10	1	US-08-192-942-7
50	8.4	30.0	10	1	US-08-777-266A-85
51	8.4	30.0	10	1	US-09-326-186B-85
52	8.4	30.0	10	1	US-09-769-482-14
53	8.4	30.0	11	1	US-08-777-266A-86
54	8.4	30.0	11	1	US-09-326-186B-86
55	8.4	30.0	11	1	US-09-249-155A-45
56	8.4	30.0	12	1	US-08-623-891-39
57	8.4	30.0	12	1	US-08-494-301A-28
58	8.4	30.0	12	1	US-08-777-266A-87
59	8.4	30.0	12	1	US-09-281-418-107
60	8.4	30.0	12	1	US-09-626-929-25
61	8.4	30.0	12	1	US-09-326-186B-87
62	8.4	30.0	12	1	US-09-484-850-25
63	8.4	30.0	12	1	US-09-408-392-25
64	8.4	30.0	12	1	US-09-626-930-25
65	8.4	30.0	12	1	US-09-626-930-25
66	8.4	30.0	12	1	US-09-340-861-39
67	8.4	30.0	12	1	US-09-634-262-39
68	8.4	30.0	12	1	US-09-626-595-25
69	8.4	30.0	12	1	US-09-694-863-25
70	8.2	29.3	21	1	US-08-702-665A-19
71	8	28.6	9	1	US-09-989-789-2038
72	8	28.6	9	1	US-08-389-789-2100
73	8	28.6	9	1	US-09-389-789-2195
74	8	28.6	9	1	US-09-989-789-2453
75	8	28.6	9	1	US-09-989-789-2454
76	8	28.6	10	1	US-08-170-095B-12
77	8	28.6	10	1	US-08-396-866-12
78	8	28.6	11	1	US-09-301-721A-12
79	8	28.6	11	1	US-09-192-707-9
80	8	28.6	12	1	US-08-086-410-4
81	8	28.6	12	1	US-07-939-501A-17
82	8	28.6	12	1	US-08-025-038-15
83	7.8	27.9	11	1	US-08-152-955-4
84	7.8	27.9	11	1	US-09-249-155A-236
85	7.8	27.9	11	1	PCT-US93-05668-4
86	7.8	27.9	12	1	US-08-035-928-19
87	7.8	27.9	12	1	US-08-435-350-107
88	7.8	27.9	12	1	US-08-494-301A-25
89	7.8	27.9	12	1	US-09-281-418-25
90	7.8	27.9	12	1	US-09-528-404-9
91	7.8	27.9	12	1	US-08-717-526-61
92	7.4	26.4	9	1	US-09-153-242-30
93	7.4	26.4	10	1	US-07-651-710A-33
94	7.4	26.4	10	1	US-07-651-710A-38
95	7.4	26.4	10	1	US-08-074-879-3
96	7.4	26.4	10	1	US-08-468-057A-3
97	7.4	26.4	10	1	US-08-378-986-6
98	7.4	26.4	10	1	US-08-388-353-495
99	7.4	26.4	10	1	US-08-388-353-495
100	7.4	26.4	10	1	US-08-388-353-657
101	7.4	26.4	10	1	US-08-388-353-658
102	7.4	26.4	10	1	US-08-388-353-661
103	7.4	26.4	10	1	US-08-388-353-661
104	7.4	26.4	10	1	US-08-488-551B-495
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106	7.4	26.4	10	1	US-08-488-551B-495



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C 109 7.4 26.4 10 1 US-08-488-551B-661 Sequence 661, App  
C 110 7.4 26.4 10 1 US-08-488-551B-662 Sequence 662, App  
C 111 7.4 26.4 10 1 US-08-488-551B-813 Sequence 813, App  
C 112 7.4 26.4 10 1 US-08-488-551B-814 Sequence 814, App  
C 113 7.4 26.4 10 1 US-08-522-384-34 Sequence 34, Appl  
C 114 7.4 26.4 10 1 US-08-488-551B-12 Sequence 12, Appl  
C 115 7.4 26.4 10 1 US-08-488-551B-17 Sequence 17, Appl  
C 116 7.4 26.4 10 1 US-08-154-750A-37 Sequence 37, Appl  
C 117 7.4 26.4 10 1 US-08-462-561B-26 Sequence 26, Appl  
C 118 7.4 26.4 10 1 US-08-301-721A-27 Sequence 27, Appl  
C 119 7.4 26.4 10 1 US-08-508-753B-160 Sequence 160, App  
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C 121 7.4 26.4 10 1 US-08-504-132-10 Sequence 10, Appl  
C 122 7.4 26.4 10 1 US-08-989-789-1630 Sequence 1630, App  
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C 124 7.4 26.4 11 1 US-07-951-715A-55 Sequence 55, Appl  
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C 128 7.4 26.4 11 1 US-08-459-444-55 Sequence 55, Appl  
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C 132 7.4 26.4 11 1 US-08-249-155A-162 Sequence 162, App  
C 133 7.4 26.4 11 1 US-08-249-155A-203 Sequence 203, App  
C 134 7.4 26.4 11 1 US-08-249-155A-231 Sequence 231, App  
C 135 7.4 26.4 18 1 US-08-633-732A-6 Sequence 6, Appl  
C 136 7.4 26.4 18 1 US-08-075-717A-6 Sequence 6, Appl  
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C 138 7.2 25.7 11 1 US-08-531-137B-35 Sequence 35, Appl  
C 139 7.2 25.7 11 1 US-08-159-765-35 Sequence 35, Appl  
C 140 7.2 25.7 11 1 US-08-796-071-35 Sequence 35, Appl  
C 141 7.2 25.7 12 1 US-08-281-418-107 Sequence 107, Appl  
C 142 7.2 25.7 12 1 US-08-281-418-25 Sequence 25, Appl  
C 143 7.2 25.7 15 1 US-08-182-968A-297 Sequence 297, App  
C 144 7.2 25.7 15 1 US-08-774-306A-297 Sequence 297, App  
C 145 7.2 25.7 15 1 US-08-064-156A-297 Sequence 297, App  
C 146 7.2 25.7 8 1 US-08-859-954-179 Sequence 179, App  
C 147 7.2 25.7 8 1 US-08-859-954-289 Sequence 289, App  
C 148 7.2 25.7 8 1 US-08-859-954-436 Sequence 436, App  
C 149 7.2 25.7 8 1 US-08-859-954-437 Sequence 437, App  
C 150 7.2 25.7 8 1 US-08-859-954-510 Sequence 510, App  
C 151 7.2 25.7 8 1 US-08-878-693-5 Sequence 5, Appl  
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C 153 7.2 25.7 9 1 US-08-605-163-11 Sequence 11, Appl  
C 154 7.2 25.7 9 1 US-08-605-163-12 Sequence 12, Appl  
C 155 7.2 25.7 9 1 US-08-331-397B-37 Sequence 37, Appl  
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C 157 7.2 25.7 9 1 US-08-046-858A-3 Sequence 3, Appl  
C 158 7.2 25.7 9 1 US-08-227-693-37 Sequence 37, Appl  
C 159 7.2 25.7 9 1 US-08-153-242-33 Sequence 33, Appl  
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C 163 7.2 25.7 9 1 US-08-989-789-2331 Sequence 2331, App  
C 164 7.2 25.7 9 1 US-08-989-789-2347 Sequence 2347, App  
C 165 7.2 25.7 9 1 US-08-989-789-2348 Sequence 2348, App  
C 166 7.2 25.7 9 1 US-08-450-513-3 Sequence 3, Appl  
C 167 7.2 25.7 10 1 US-08-263-790-19 Sequence 19, Appl  
C 168 7.2 25.7 10 1 US-08-538-341-12 Sequence 12, Appl  
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C 171 7.2 25.7 10 1 US-08-590-571-19 Sequence 19, Appl  
C 172 7.2 25.7 10 1 US-08-590-571-31 Sequence 31, Appl  
C 173 7.2 25.7 10 1 US-08-388-353-659 Sequence 659, App  
C 174 7.2 25.7 10 1 US-08-388-353-660 Sequence 660, App  
C 175 7.2 25.7 10 1 US-08-468-856B-14 Sequence 14, Appl  
C 176 7.2 25.7 10 1 US-08-488-551B-659 Sequence 659, App  
C 177 7.2 25.7 10 1 US-08-488-551B-660 Sequence 660, App  
C 178 7.2 25.7 10 1 US-08-468-859A-14 Sequence 14, Appl  
C 179 7.2 25.7 10 1 US-08-906-691-10 Sequence 10, Appl

C 180 7 25.0 10 1 US-08-522-384-27 Sequence 27, Appl  
C 181 7 25.0 10 1 US-08-154-750A-49 Sequence 49, Appl  
C 182 7 25.0 10 1 US-08-313-221A-136 Sequence 136, App  
C 183 7 25.0 10 1 US-08-537-186-13 Sequence 13, Appl  
C 184 7 25.0 10 1 US-08-508-753B-151 Sequence 151, App  
C 185 7 25.0 10 1 US-10-042-111-31 Sequence 31, Appl  
C 186 7 25.0 10 1 US-08-538-456-9 Sequence 9, Appl  
C 187 7 25.0 10 1 US-08-769-482-43 Sequence 43, Appl  
C 188 7 25.0 10 1 US-08-989-789-1385 Sequence 1285, App  
C 189 7 25.0 10 1 US-08-989-789-1397 Sequence 1397, App  
C 190 7 25.0 10 1 US-08-263-790-19 Sequence 19, Appl  
C 191 6.8 24.3 10 1 US-08-538-341-12 Sequence 12, Appl  
C 192 6.8 24.3 10 1 US-08-785-716A-18 Sequence 18, Appl  
C 193 6.8 24.3 10 1 US-08-789-880-19 Sequence 19, Appl  
C 194 6.8 24.3 10 1 US-08-388-353-660 Sequence 660, App  
C 195 6.8 24.3 10 1 US-08-488-551B-660 Sequence 660, App  
C 196 6.8 24.3 10 1 US-08-537-186-13 Sequence 13, Appl  
C 197 6.8 24.3 10 1 US-08-538-456-9 Sequence 9, Appl  
C 198 6.8 24.3 10 1 US-08-474-177-23 Sequence 23, Appl  
C 199 6.6 23.6 16 1 US-08-487-033-23 Sequence 23, Appl  
C 200 6.6 23.6 16 1 US-08-480-810-23 Sequence 23, Appl  
C 201 6.6 23.6 16 1 US-08-508-735-23 Sequence 23, Appl  
C 202 6.6 23.6 16 1 US-08-848-251-23 Sequence 23, Appl  
C 203 6.6 23.6 16 1 US-08-486-047-23 Sequence 23, Appl  
C 204 6.6 23.6 16 1 US-08-120-130-23 Sequence 23, Appl  
C 205 6.6 23.6 16 1 US-08-115-252-23 Sequence 23, Appl  
C 206 6.6 23.6 16 1 US-08-986-515-23 Sequence 23, Appl  
C 207 6.6 23.6 16 1 US-08-120-128-23 Sequence 23, Appl  
C 208 6.6 23.6 16 1 US-08-120-129-23 Sequence 23, Appl  
C 209 6.6 23.6 16 1 US-08-201-139-23 Sequence 23, Appl  
C 210 6.6 23.6 16 1 US-08-120-131-23 Sequence 34, Appl  
C 211 6.4 22.9 10 1 US-08-522-384-34 Sequence 34, Appl  
C 212 6.4 22.9 10 1 US-08-425-798-12 Sequence 12, Appl  
C 213 6.4 22.9 10 1 US-08-319-492B-24 Sequence 24, Appl  
C 214 6.2 22.1 15 1 US-08-989-789-2453 Sequence 2453, App  
C 215 6 21.4 9 1 US-08-989-789-2454 Sequence 2454, App  
C 216 6 21.4 9 1 US-08-153-242-30 Sequence 30, Appl  
C 217 6 21.4 9 1 US-08-153-242-33 Sequence 33, Appl  
C 218 6 21.4 9 1 US-08-153-242-33 Sequence 33, Appl

ALIGNMENTS

US-08-702-665A-19  
Sequence 19, Application US/08702665A  
Patent No. 6274708  
GENERAL INFORMATION:  
APPLICANT: Hilton, Douglas J.  
TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States of America  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08702.665A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Presser, Leopold  
REGISTRATION NUMBER: 19,827  
REFERENCE/DOCKET NUMBER: 10296  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 203 901 SANS UR  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-702-665A-19

Query Match 50.7%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 3.7;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTGACAGGAGTCCAG 28  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3 CCTGACTGGAGTCCAG 21

RESULT 2  
US-08-633-792A-6/C  
; Sequence 6, Application US/08633792A  
; Patent No. 5837694  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Graham L  
; TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE SURVIVAL  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/633,792A  
; FILING DATE: 01-JUL-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PM/1870  
; FILING DATE: 18-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 10062  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4366  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA oligonucleotide"  
US-08-633-792A-6

Query Match 47.9%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 4.5;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCA 26  
| | | | | | | | | | | | | | | | | | | | | |  
Db 17 TGTACAGGAGTCCA 3

Db 17 TGTACAGGAGTCCA 3

RESULT 3  
US-09-075-717A-6/c  
; Sequence 6, Application US/09075717A  
; Patent No. 6174869  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Graham L  
; TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE SURVIVAL  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/075,717A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/633,792  
; FILING DATE: 01-JUL-1996  
; APPLICATION NUMBER: AU PM/1870  
; FILING DATE: 18-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 10062  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA oligonucleotide"  
US-09-075-717A-6

Query Match 47.9%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 4.5;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCA 26  
| | | | | | | | | | | | | | | | | | | | | |  
Db 17 TGTACAGGAGTCCA 3

RESULT 4  
US-08-630-592-18  
; Sequence 18, Application US/08630592  
; Patent No. 5770432  
; GENERAL INFORMATION:  
; APPLICANT: Nishina, Patsy  
; APPLICANT: No. 5770432entrauth, Konrad  
; APPLICANT: Nagger, Juergen  
; APPLICANT: No. 5770432th, Michael  
; TITLE OF INVENTION: Obesity Associated Genes  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT

STREET: 3400 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,592

FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J.  
REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: A59504/BIR/PJS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 7811989  
TELEFAX: (415) 3983249  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
US-08-630-592-18

Query Match 44.3%; Score 12.4; DB 1; Length 19;  
Best Local Similarity 92.9%; Pred. No. 10;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAGG 28  
|||||  
Db 6 ACAGGGAGACCAGG 19

RESULT 5  
US-08-714-991-18  
Sequence 18, Application US/08714991  
Patent No. 5776762  
GENERAL INFORMATION:  
APPLICANT: NORTON, Michael  
APPLICANT: NISHINA, Patsy  
APPLICANT: No. 5776762en-Trauth, Konrad  
APPLICANT: NAGERT, Juergen  
TITLE OF INVENTION: OBESITY ASSOCIATED GENES  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/714,991  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SHERWOOD, Pamela J.  
REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: A-59504-1/PJS  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-494-8700  
TELEFAX: 415-494-8771  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
US-08-714-991-18

Query Match 44.3%; Score 12.4; DB 1; Length 19;  
Best Local Similarity 92.9%; Pred. No. 10;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAGG 28  
|||||  
Db 6 ACAGGGAGACCAGG 19

RESULT 6  
US-09-032-365A-30  
Sequence 30, Application US/09032365A  
Patent No. 6114502  
GENERAL INFORMATION:  
APPLICANT: No. 6114502th, Michael  
APPLICANT: Nishina, Patsy  
APPLICANT: Naggart, Juergen  
APPLICANT: No. 6114502en-Trauth, Konrad  
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bozicevic & Reed, LLP  
STREET: 285 Hamilton Avenue, Suite 200  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,365A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J.  
REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: SEQ-2CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-327-3400  
TELEFAX: 650-327-3231  
TELEX:  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-032-365A-30

Query Match 44.3%; Score 12.4; DB 1; Length 19;  
Best Local Similarity 92.9%; Pred. No. 10;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAGG 28  
| | | | | | | | | |  
DB 6 ACAGGGAGTCCAGG 19

## RESULT 7

US-08-117-952-129/c  
; Sequence 129, Application US/08117952  
; Patent No. 5851760  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Glen A.  
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE  
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES  
; NUMBER OF SEQUENCES: 797  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/117,952  
; FILING DATE: 07-SEP-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/078,471  
; FILING DATE: 15-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: P41 9423  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-4737  
; TELEFAX: 619-546-9392  
; INFORMATION FOR SEQ ID NO: 129:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Oligonucleotide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-117-952-129

Query Match 43.6%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 10;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGTCCAG 27  
| | | | | | | | | |  
DB 18 GTGTACAGGAGTCCAG 2

## RESULT 8

US-08-970-269A-6  
; Sequence 6, Application US/08970269A  
; Patent No. 5976803  
; GENERAL INFORMATION:  
; APPLICANT: Kathryn Meek  
; TITLE OF INVENTION: Genetic Test For Equine Severe  
; TITLE OF INVENTION: Combined Immunodeficiency Disease  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Benjamin A. Adler

STREET: 8011 Candle Lane  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77071

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple  
OPERATING SYSTEM: Macintosh  
SOFTWARE: Microsoft Word for Macintosh  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970,269A  
FILING DATE: No. 5976803ember 14, 1997  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Adler Ph.D., Benjamin A.  
REGISTRATION NUMBER: 35,423  
REFERENCE/DOCKET NUMBER: D5860  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-777-2321  
TELEFAX: 713-777-6908

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: no  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
FEATURE:

US-08-970-269A-6

Query Match 43.6%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 10;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCAGG 28  
| | | | | | | | | |  
DB 1 TGTACAGGAGTCCAGG 17

## RESULT 9

US-03-407-562-6  
; Sequence 6, Application US/09407562  
; Patent No. 6294334  
; GENERAL INFORMATION:  
; APPLICANT: Kathryn Meek  
; TITLE OF INVENTION: Genetic Test For Equine Severe  
; TITLE OF INVENTION: Combined Immunodeficiency Disease  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Benjamin A. Adler  
; STREET: 8011 Candle Lane  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77071

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple  
OPERATING SYSTEM: Macintosh  
SOFTWARE: Microsoft Word for Macintosh  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/407,562  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/970,269  
FILING DATE: No. 6294334ember 14, 1997  
CLASSIFICATION:

```
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: no
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
FEATURE:
US-09-407-562-6

Query Match 43.6%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TCTACAGGAGTCCAGG 28
DB 1 TCTACAGGGAATTCAGG 17

RESULT 10
US-08-474-177-23
Sequence 23, Application US/08474177
Patent No. 5624819
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-474-177-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGTGTACAGGAGTCC 25
DB 1 CGTGTCCAGGAGCCC 16

RESULT 11
US-08-487-033-23
Sequence 23, Application US/08487033
Patent No. 5739027
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1E1-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
```

NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-487-033-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 15;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25  
|||||  
DB 1 CGGTCCAGGAGCCC 16

RESULT 12  
US-08-480-810-23  
Sequence 23, Application US/08480810  
Patent No. 5801236  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,810  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-480-810-23  
Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 15;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 10 CGGTACAGGAGTCC 25  
|||||  
DB 1 CGGTCCAGGAGCCC 16  
RESULT 13  
US-08-508-735-23  
Sequence 23, Application US/08508735  
Patent No. 5843756  
GENERAL INFORMATION:  
APPLICANT: Stone, Steven  
APPLICANT: Jiang, Ping  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/508,735  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US to be assigned  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-8300  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO

ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-508-735-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 15;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTGACAGGAGTCC 25  
Db 1 CGGTGACAGGAGGCC 16

RESULT 14

US-08-848-251-23  
Sequence 23, Application US/08848251  
Patent No. 5989815

GENERAL INFORMATION:

APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND  
METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS  
TITLE OF INVENTION: GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/848,251  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/474,083  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-G  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-848-251-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 15;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTGACAGGAGTCC 25  
Db 1 CGGTGACAGGAGGCC 16

RESULT 15

US-08-486-047-23  
Sequence 23, Application US/08486047  
Patent No. 5994095

GENERAL INFORMATION:

APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS2 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/486,047  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-B  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-486-047-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 15;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25  
|||||  
Db 1 CGGTCCAGGAGCCC 16

## RESULT 16

US-09-120-130-23  
Sequence 23, Application US/09120130  
Patent No. 6037462  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/120,130  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480,810  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELEPHONE: 202-962-8300  
TELEFAX: 202-962-4810

INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO

ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-120-130-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 15;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25  
|||||  
Db 1 CGGTCCAGGAGCCC 16

## RESULT 17

US-09-115-252-23  
Sequence 23, Application US/09115252  
Patent No. 6060301  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/115,252  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,810  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO



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/ ANTI-SENSE: YES
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
US-09-115-252-23
Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred.No.15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
| | | | | | | | | | | | | | | |
Db 1 CGGTCCAGGAGGCC 16

RESULT 18
US-08-986-515-23
; Sequence 23, Application US/08986515
; Patent No. 6090578
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,810
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:

/ ANTI-SENSE: YES
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
US-08-986-515-23
Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred.No.15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
| | | | | | | | | | | | | | | |
Db 1 CGGTCCAGGAGGCC 16

RESULT 19
US-09-120-128-23
; Sequence 23, Application US/09120128
; Patent No. 6140473
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,128
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,047
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
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ORGANISM:	Homo sapiens	Score 11.2;	DB 1;	Length 16;
US-09-120-129-23	40.0%;	81.2%;	Pred. No. 15;	Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Query Match	40.0%;	81.2%;	Pred. No. 15;	Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Best Local Similarity	81.2%;	81.2%;	Pred. No. 15;	Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	10	CGGTGTACAGGAGTCC	25	
DB	1	CGGTGTCCAGGAGGCC	16	
RESULT 20				
US-09-120-129-23				
Sequence 23, Application US/09120129				
Patent No. 6180776				
GENERAL INFORMATION:				
APPLICANT: Kamb, Alexander				
TITLE OF INVENTION: M152 GENE				
NUMBER OF SEQUENCES: 36				
CORRESPONDENCE ADDRESS:				
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP				
STREET: 1201 New York Avenue, Suite 1000				
CITY: Washington				
STATE: DC				
COUNTRY: USA				
ZIP: 20005				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Floppy disk				
COMPUTER: IBM PC compatible				
OPERATING SYSTEM: PC-DOS/MS-DOS				
SOFTWARE: Patent In Release #1.0, Version #1.30				
CURRENT APPLICATION DATA:				
APPLICATION NUMBER: US/09/120,129				
FILING DATE:				
CLASSIFICATION:				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 08/486,047				
FILING DATE: 07-JUN-1995				
APPLICATION NUMBER: PCT/US95/03316				
FILING DATE: 17-MAR-1995				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 08/251,938				
FILING DATE: 01-JUN-1994				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 08/215,087				
FILING DATE: 18-MAR-1994				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 08/215,086				
FILING DATE: 18-MAR-1994				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 08/227,369				
FILING DATE: 14-APR-1994				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 08/214,562				
FILING DATE: 18-MAR-1994				
ATTORNEY/AGENT INFORMATION:				
NAME: Ihnen, Jeffrey L.				
REGISTRATION NUMBER: 28,957				
REFERENCE/DOCKET NUMBER: 24884-109348-B				
TELECOMMUNICATION INFORMATION:				
TELEPHONE: 202-962-4810				
TELEFAX: 202-962-8300				
INFORMATION FOR SEQ ID NO: 23:				
SEQUENCE CHARACTERISTICS:				
LENGTH: 16 base pairs				
TYPE: nucleic acid				
STRANDEDNESS: single				
TOPOLOGY: linear				
MOLECULE TYPE: DNA (genomic)				
HYPOTHETICAL: NO				
ANTI-SENSE: YES				
ORIGINAL SOURCE:				
ORGANISM: Homo sapiens				
US-09-120-129-23				
Query Match	40.0%;	81.2%;	Pred. No. 15;	Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Best Local Similarity	81.2%;	81.2%;	Pred. No. 15;	Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	10	CGGTGTACAGGAGTCC	25	
DB	1	CGGTGTCCAGGAGGCC	16	
RESULT 21				
US-09-201-139-23				
Sequence 23, Application US/09201139				
Patent No. 6210949				
GENERAL INFORMATION:				
APPLICANT: Stone, Steven				
TITLE OF INVENTION: M152 GENE				
NUMBER OF SEQUENCES: 47				
CORRESPONDENCE ADDRESS:				
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP				
STREET: 1201 New York Avenue, Suite 1000				
CITY: Washington				
STATE: DC				
COUNTRY: USA				
ZIP: 20005				</

ORGANISM:	Homo sapiens	Score 11.2;	DB 1;	Length 16;
US-09-120-129-23	40.0%;	81.2%;	Pred. No. 15;	Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Query Match	40.0%;	81.2%;	Pred. No. 15;	Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Best Local Similarity	81.2%;	81.2%;	Pred. No. 15;	Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	10	CGGTGTACAGGAGTCC	25	
DB	1	CGGTGTCCAGGAGGCC	16	
RESULT 20				
US-09-120-129-23				
Sequence 23, Application US/09120129				
Patent No. 6180776				
GENERAL INFORMATION:				
APPLICANT: Kamb, Alexander				
TITLE OF INVENTION: M152 GENE				
NUMBER OF SEQUENCES: 36				
CORRESPONDENCE ADDRESS:				
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP				
STREET: 1201 New York Avenue, Suite 1000				
CITY: Washington				
STATE: DC				
COUNTRY: USA				
ZIP: 20005				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Floppy disk				
COMPUTER: IBM PC compatible				
OPERATING SYSTEM: PC-DOS/MS-DOS				
SOFTWARE: Patent In Release #1.0, Version #1.30				
CURRENT APPLICATION DATA:				
APPLICATION NUMBER: US/09/120,129				
FILING DATE:				
CLASSIFICATION:				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 08/486,047				
FILING DATE: 07-JUN-1995				
APPLICATION NUMBER: PCT/US95/03316				
FILING DATE: 17-MAR-1995				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 08/251,938				
FILING DATE: 01-JUN-1994				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 08/215,087				
FILING DATE: 18-MAR-1994				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 08/215,086				
FILING DATE: 18-MAR-1994				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 08/227,369				
FILING DATE: 14-APR-1994				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 08/214,562				
FILING DATE: 18-MAR-1994				
ATTORNEY/AGENT INFORMATION:				
NAME: Ihnen, Jeffrey L.				
REGISTRATION NUMBER: 28,957				
REFERENCE/DOCKET NUMBER: 24884-109348-B				
TELECOMMUNICATION INFORMATION:				
TELEPHONE: 202-962-4810				
TELEFAX: 202-962-8300				
INFORMATION FOR SEQ ID NO: 23:				
SEQUENCE CHARACTERISTICS:				
LENGTH: 16 base pairs				
TYPE: nucleic acid				
STRANDEDNESS: single				
TOPOLOGY: linear				
MOLECULE TYPE: DNA (genomic)				
HYPOTHETICAL: NO				
ANTI-SENSE: YES				
ORIGINAL SOURCE:				
ORGANISM: Homo sapiens				
US-09-120-129-23				
Query Match	40.0%;	81.2%;	Pred. No. 15;	Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Best Local Similarity	81.2%;	81.2%;	Pred. No. 15;	Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	10	CGGTGTACAGGAGTCC	25	
DB	1	CGGTGTCCAGGAGGCC	16	



COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,306A  
FILING DATE: December 26, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/182,968  
FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882,888  
FILING DATE: May 14, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 227/227  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-774-306A-121

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 17;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15  
|||||:|:|  
DB 1 GGGCCCUCCGUGCA 14

RESULT 25  
US-09-064-156A-121  
Sequence 121, Application US/09064156A  
Patent No. 6132966  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 498  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/064,156A  
FILING DATE: April 21, 1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/774,306  
FILING DATE: December 26, 1996  
APPLICATION NUMBER: 08/182,968  
FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882,888  
FILING DATE: May 14, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 234/083  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-064-156A-121

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 17;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15  
|||||:|:|  
DB 1 GGGCCCUCCGUGCA 14

RESULT 26  
US-09-081-646-637/c  
Sequence 637, Application US/09081646  
Patent No. 633152  
GENERAL INFORMATION:  
APPLICANT: Kinzler, Kenneth  
APPLICANT: Vogelstein, Bert  
APPLICANT: Zhang, Lin  
APPLICANT: Zhou, Wei  
TITLE OF INVENTION: Gene Expression Profiles in No. 633152mal and  
FILE REFERENCE: 01107.74664  
CURRENT APPLICATION NUMBER: US/09/081,646  
CURRENT FILING DATE: 1998-05-20  
EARLIER APPLICATION NUMBER: 60/047,352  
EARLIER FILING DATE: 1997-05-21  
NUMBER OF SEQ ID NOS: 871  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 637  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-081-646-637

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 17;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAGG 28  
|||||:|:|  
DB 14 ACAGAGAGTCCATG 1

RESULT 27  
US-09-180-437-185  
Sequence 185, Application US/09180437  
Patent No. 6251873  
GENERAL INFORMATION:  
APPLICANT: FUKUSAKO, Shioji  
APPLICANT: MORISAWA, Yoshifumi  
APPLICANT: KUSUYAMA, Takeshi  
TITLE OF INVENTION: Antisense Compounds to CD14  
FILE REFERENCE: 1110-209P  
CURRENT APPLICATION NUMBER: US/09/180,437  
CURRENT FILING DATE: 1998-11-06  
EARLIER APPLICATION NUMBER: PCT/JP98/00953  
EARLIER FILING DATE: 1998-03-09  
EARLIER APPLICATION NUMBER: 09-053518 JAPAN

EARLIER FILING DATE: 1997-03-07  
NUMBER OF SEQ ID NOS: 289  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 185  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: other nucleic  
OTHER INFORMATION: acid  
US-09-180-437-185

Query Match 37.1%; Score 10.4; DB 1; Length 15;  
Best Local Similarity 91.7%; Pred. No. 23;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 AGGGAGTCCAGG 28  
|||||  
DB 4 AGGGAGTTCAGG 15

RESULT 28  
US-08-182-968A-297  
Sequence 297, Application US/08182968A  
Patent No. 5610054  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 497  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,968A  
FILING DATE: 13-JANUARY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,888  
FILING DATE: 14-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 205/277  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 297:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-182-968A-297  
Query Match 35.7%; Score 10; DB 1; Length 15;  
Best Local Similarity 90.0%; Pred. No. 29;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28  
|||||

Db 3 GGAGUCCAGG 12

RESULT 29

US-08-319-492B-24  
Sequence 24, Application US/08319492B  
Patent No. 5616488  
GENERAL INFORMATION:  
APPLICANT: Sullivan, Sean M.  
APPLICANT: Draper, Kenneth G.  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF IL-5  
NUMBER OF SEQUENCES: 751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,492B  
FILING DATE: October 7, 1994  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-319-492B-24  
Query Match 35.7%; Score 10; DB 1; Length 15;  
Best Local Similarity 70.0%; Pred. No. 29;  
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Two

QY 6 CCTACGTGTA 15  
|||||

Db 5 CCUACGUGUA 14

RESULT 30

US-08-774-306A-297  
Sequence 297, Application US/08774306A  
Patent No. 5869253  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HEPATITIS C

```
;
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,306A
; FILING DATE: December 26, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 297:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-774-306A-297

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 90.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
Db 3 GGAGUCCAGG 12

RESULT 31
US-09-064-156A-297
; Sequence 297, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,156A
; FILING DATE: April 21, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 297:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-064-156A-297

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 90.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
Db 3 GGAGUCCAGG 12

RESULT 32
US-09-698-505A-38/c
; Sequence 38, Application US/09698505A
; Patent No. 6479242
; GENERAL INFORMATION:
; APPLICANT: Guo, Baochuan
; TITLE OF INVENTION: A NO. 6479242a1 Method for Genotyping of Single Nucleotide Polym
; FILE REFERENCE: 27433/04001
; CURRENT APPLICATION NUMBER: US/09/698,505A
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 14
; TYPE: DNA
; ORGANISM: A Homozygote
; US-09-698-505A-38

Query Match 35.0%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 29;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTC 24
Db 14 TGGCAGGAGTC 2

RESULT 33
US-08-182-968A-115
; Sequence 115, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,968A  
FILING DATE: 13-JANUARY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,888  
FILING DATE: 14-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 205/277  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 115:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;  
Best Local Similarity 61.5%; Pred. No. 33;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15  
| | | | | : :  
Db 2 GCCCUACGUUA 14

RESULT 34  
US-08-774-306A-115  
; Sequence 115, Application US/08774306A  
; Patent No. 5869253  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HEPATITIS C  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 497  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/774.306A  
; FILING DATE: December 26, 1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/182,968

FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882,888  
FILING DATE: May 14, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 223/227  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 115:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-774-306A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;  
Best Local Similarity 61.5%; Pred. No. 33;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15  
| | | | | : :  
Db 2 GCCCUACGUUA 14

RESULT 35  
US-09-064-156A-115  
; Sequence 115, Application US/09064156A  
; Patent No. 6132966  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HEPATITIS C  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 498  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/064,156A  
; FILING DATE: April 21, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/774,306  
; FILING DATE: December 26, 1996  
; APPLICATION NUMBER: 08/182,968  
; FILING DATE: January 13, 1994  
; APPLICATION NUMBER: 07/882,888  
; FILING DATE: May 14, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 234/083  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15

```
;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-064-156A-115

Query Match      35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTA 15
   |||||:
Db 2 GCCCTACGUAUA 14

RESULT 36
US-09-180-437-134/c
; Sequence 134, Application US/09180437
; Patent No. 6251873
; GENERAL INFORMATION:
; APPLICANT: FUKUSAKO, Shioji
; APPLICANT: MORISAWA, Yoshifumi
; APPLICANT: KUSUYAMA, Takeshi
; TITLE OF INVENTION: Antisense Compounds to CD14
; FILE REFERENCE: 1110-209P
; CURRENT APPLICATION NUMBER: US/09/180,437
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: PCT/JP98/00953
; EARLIER FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: 09-053518 JAPAN
; EARLIER FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 134
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
US-09-180-437-134

Query Match      35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 33;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGT 14
   |||||
Db 13 GCGCCCTGCGTGT 1

RESULT 37
PCT-US93-02612-2/c
; Sequence 2, Application PC/TUS9302612
; GENERAL INFORMATION:
; APPLICANT: Cable, Michael
; APPLICANT: Hesson, Thomas
; APPLICANT: Mannarino, Anthony
; TITLE OF INVENTION: Monomeric Platelet-Derived Growth Factor and Prevention of
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 4.00B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02612
```

```
;
; FILING DATE: 19930326
; CLASSIFICATION:
; PRIOR APPLICATION DATA: None
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G.
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: JB0255
; TELEPHONE: 201-822-7255
; TELEFAX: 201-822-7039
; TELEX: 219165
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US93-02612-2

Query Match      35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 33;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 CAGGGAGTCCAGG 28
   |||||
Db 15 CAGGGAACCCAGG 3

RESULT 38
US-09-203-231B-67
; Sequence 67, Application US/09203231B
; Patent No. 6355423
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/203,231B
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/105,305
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-203-231B-67

Query Match      33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCTACGTGTAC 16
   |||||
Db 2 CCTACGTGTAC 12

RESULT 39
5174962-2
; Patent No. 5174962
; APPLICANT: BRENNAN, THOMAS M.
; TITLE OF INVENTION: APPARATUS FOR DETERMINING DNA SEQUENCES
; BY MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/459,728
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
```



; APPLICATION NUMBER: 209,247  
; FILING DATE: 20-JUN-1988  
; SEQ ID NO:2  
; LENGTH: 12  
5174962-2

Query Match 33.6%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 27;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 ACGTGTACAGG 19  
|||||  
DB 1 ACGTGTACAG 11

RESULT 40  
5174962-2/c  
; Patent No. 5174962  
; APPLICANT: BRENNAN, THOMAS M.  
; TITLE OF INVENTION: APPARATUS FOR DETERMINING DNA SEQUENCES  
; BY MASS SPECTROMETRY  
; NUMBER OF SEQUENCES: 2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/459,728  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 209,247  
; FILING DATE: 20-JUN-1988  
; SEQ ID NO:2  
; LENGTH: 12  
5174962-2

Query Match 33.6%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 27;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 ACGTGTACAGG 19  
|||||  
DB 12 ACGTGTACAG 2

RESULT 41  
US-08-623-891-20/c  
; Sequence 20, Application US/08623891  
; Patent No. 5795778  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; OPERATING SYSTEM: INHIBITING HERPES SIMPLEX  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 115  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/623,891  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/238,200  
; FILING DATE:  
; APPLICATION NUMBER: US/07/987,133  
; FILING DATE:  
; APPLICATION NUMBER: 07/882,921

; FILING DATE: May 14, 1992  
; APPLICATION NUMBER: 07/948,359  
; FILING DATE: September 18, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 200/209  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-623-891-20

Query Match 32.9%; Score 9.2; DB 1; Length 14;  
Best Local Similarity 78.6%; Pred. No. 42;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGTGATCAGGGAGT 23  
|||||  
DB 14 CGTGATCAGGGAGT 1

RESULT 42  
US-05-340-861-20/c  
; Sequence 20, Application US/09340861  
; Patent No. 6432704  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; OPERATING SYSTEM: INHIBITING HERPES SIMPLEX  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 115  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/340,861  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/987,133  
; FILING DATE:  
; APPLICATION NUMBER: 07/882,921  
; FILING DATE: May 14, 1992  
; APPLICATION NUMBER: 07/948,359  
; FILING DATE: September 18, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 200/209  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14  
; TYPE: nucleic acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-340-861-20

Query Match      32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 42;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 CGGTACAGGAGT 23
Db 14 CGTGATCAGGGCGT 1

RESULT 43
US-09-634-262-20/c
; Sequence 20, Application US/09634262
; Patent No. 6440719
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/634,262
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELETYPE: 67-3510
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-634-262-20

Query Match      32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 42;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 CGGTACAGGAGT 23
Db 14 CGTGATCAGGGCGT 1

RESULT 44
US-08-494-301A-6/c
; Sequence 6, Application US/08494301A
; Patent No. 5856461
; GENERAL INFORMATION:
; APPLICANT: Colote, Soudhir
; APPLICANT: Pirotzky, Eduardo
; TITLE OF INVENTION: Oligonucleotides to Inhibit the
; TITLE OF INVENTION: Expression of Isoprenyl Protein Transferases
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lucas & Just
; STREET: 205 E. 42nd Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,
; MEDIUM TYPE: 1.44 MB storage
; COMPUTER: IBM 486 Compatible
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,301A
; FILING DATE: 23-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9413035.8
; FILING DATE: 29-JUNE-1994
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: Yes
US-08-494-301A-6

Query Match      32.1%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GTACAGGGA 21
Db 12 GTACAGGGA 4

RESULT 45
US-09-203-231B-67/c
; Sequence 67, Application US/09203231B
; Patent No. 6355423
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/203,231B
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/105,305
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-203-231B-67

Query Match      31.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 40;
```

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Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 13 GTACAGGAGTC 24
DB 12 GTACAGGTAGGC 1

RESULT 46
US-09-281-418-211/c
; Sequence 211, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
; TITLE OF INVENTION: agent, Method of Assaying Microorganisms, Method of Analyzing Mi
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281.418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 211
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-211

Query Match 31.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCTACGTGTAC 16
DB 12 CCATACGTGCAC 1

RESULT 47
US-09-014-304-3
; Sequence 3, Application US/09014304
; Patent No. 6063573
; GENERAL INFORMATION:
; APPLICANT: Kayem, Jon Faiz
; TITLE OF INVENTION: Cycling Probe Technology Using Electron Transfer
; TITLE OF INVENTION: Detection
; FILE REFERENCE: A65687/RFT/RMS/RVK
; CURRENT APPLICATION NUMBER: US/09/014,304
; CURRENT FILING DATE: 1998-01-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-014-304-3

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 ACGTGACAGG 20
DB 1 ACGTGCCATGG 12

RESULT 48
US-09-874-601-30

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; Sequence 30, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHC
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 30
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-30

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGCGCCTACGT 12
DB 1 CAGGCUCUACGU 12

RESULT 49
US-08-192-942-7/c
; Sequence 7, Application US/08192942
; Patent No. 5989906
; GENERAL INFORMATION:
; APPLICANT: JAMES D. THOMPSON
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING P-GLYCOPROTEIN mdr-
; TITLE OF INVENTION: 1 GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/192,942
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/882,885
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/173
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600

```

TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-192-942-7  
Query Match 30.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 35;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 18 GGGAGTCCAG 27  
DB 10 GGAAGTCCAG 1  
RESULT 50  
US-08-777-266A-85/c  
Sequence 85, Application US/08777266A  
Patent No. 6077833  
GENERAL INFORMATION:  
APPLICANT: Clarence Frank Bennett  
APPLICANT: Timothy A. Vickers  
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Expression of B7 Proteins  
TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,266A  
FILING DATE: December 31, 1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-08-777-266A-85  
Query Match 30.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 35;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 13 GTACAGGGAG 22  
DB 10 GTACAGGGAG 1

RESULT 51  
US-09-326-186B-85/c  
Sequence 85, Application US/09326186B  
Patent No. 6319906  
GENERAL INFORMATION:  
APPLICANT: Bennett, Clarence Frank  
APPLICANT: Vickers, Timothy A.  
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the  
TITLE OF INVENTION: Modulation of the Expression of B7 Protein  
FILE REFERENCE: ISPH-0376  
CURRENT APPLICATION NUMBER: US/09/326,186B  
CURRENT FILING DATE: 1999-06-04  
PRIOR APPLICATION NUMBER: 08/777,266  
PRIOR FILING DATE: 1996-12-31  
NUMBER OF SEQ ID NOS: 226  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 85  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-326-186B-85  
Query Match 30.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 35;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 13 GTACAGGGAG 22  
DB 10 GTACAGGGAG 1  
RESULT 52  
US-09-769-482-14  
Sequence 14, Application US/09769482  
Patent No. 6566130  
GENERAL INFORMATION:  
APPLICANT: SRIVASTAVA, SHIV  
APPLICANT: MOUL, JUDD W.  
APPLICANT: XU, LINDA L.  
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED  
TITLE OF INVENTION: POYNUCLEOTIDE ARRAY  
FILE REFERENCE: 04995.0057-00000  
CURRENT APPLICATION NUMBER: US/09/769,482  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/178,772  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/179,045  
PRIOR FILING DATE: 2000-01-31  
NUMBER OF SEQ ID NOS: 67  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 14  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: oligonucleotide  
US-09-769-482-14  
Query Match 30.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 35;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 13 GTACAGGGAG 22  
DB 1 GTGACGGGAG 10  
RESULT 53  
US-08-777-266A-86/c

; Sequence 86, Application US/0877266A  
; Patent No. 6077833  
; GENERAL INFORMATION:  
; APPLICANT: Clarence Frank Bennett  
; APPLICANT: Timothy A. Vickers  
; TITLE OF INVENTION: Oligonucleotide Compositions and  
; TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins  
; NUMBER OF SEQUENCES: 125  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Law Offices of Jane Massey Licata  
; STREET: 210 Lake Drive East, Suite 201  
; CITY: Cherry Hill  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION NUMBER: US/08/777,266A  
; FILING DATE: December 31, 1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane Massey Licata  
; REGISTRATION NUMBER: 32,257  
; REFERENCE/DOCKET NUMBER: ISPH-0201  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (609) 779-2400  
; TELEFAX: (609) 779-8488  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE: Yes  
US-08-777-266A-86

Query Match 30.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 43;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GTACAGGGAG 22  
DB 11 GTACGGGGAG 2

RESULT 54  
US-09-326-186B-86/c  
; Sequence 86, Application US/09326186B  
; Patent No. 6319906  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Clarence Frank  
; APPLICANT: Vickers, Timothy A.  
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the  
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein  
; FILE REFERENCE: ISPH-0376  
; CURRENT APPLICATION NUMBER: US/09/326,186B  
; CURRENT FILING DATE: 1999-06-04  
; PRIOR APPLICATION NUMBER: 08/777,266  
; PRIOR FILING DATE: 1996-12-31  
; NUMBER OF SEQ ID NOS: 226  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 86  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Synthetic  
US-09-326-186B-86

Query Match 30.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 43;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GTACAGGGAG 22  
DB 11 GTACGGGGAG 2

RESULT 55  
US-09-249-155A-45/c  
; Sequence 45, Application US/09249155A  
; Patent No. 6538173  
; GENERAL INFORMATION:  
; APPLICANT: Heber-Katz, Ellen  
; TITLE OF INVENTION: Compositions and Methods for Wound  
; TITLE OF INVENTION: Healing  
; FILE REFERENCE: 00486.78503  
; CURRENT APPLICATION NUMBER: US/09/249,155A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,737  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/097,937  
; PRIOR FILING DATE: 1998-08-26  
; PRIOR APPLICATION NUMBER: US 60/102,051  
; PRIOR FILING DATE: 1998-09-28  
; NUMBER OF SEQ ID NOS: 346  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-249-155A-45

Query Match 30.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 43;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACGGGA 21  
DB 10 TGTACGGGGA 1

RESULT 56  
US-08-623-891-39  
; Sequence 39, Application US/08623891  
; Patent No. 5795778  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 115  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/623,891  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/238,200  
FILING DATE: US/07/987,133  
FILING DATE: US/07/987,133  
APPLICATION NUMBER: 07/882,921  
FILING DATE: May 14, 1992  
APPLICATION NUMBER: 07/948,359  
FILING DATE: September 18, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 200/209  
REFERENCE/DOCKET NUMBER: 200/209  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-623-891-39

Query Match 30.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 70.0%; Pred. No. 51;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCTACGTGT 14  
Db 1 CCGACGUGU 10

## RESULT 57

US-08-494-301A-28/c  
Sequence 28, Application US/08/494301A  
Patent No. 5856461  
GENERAL INFORMATION:  
APPLICANT: Colote, Soudhir  
APPLICANT: Colote, Soudhir  
TITLE OF INVENTION: Oligonucleotides to Inhibit the  
TITLE OF INVENTION: Expression of Isoprenyl Protein Transferases  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lucas & Just  
STREET: 205 E. 42nd Street  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10017

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch,  
MEDIUM TYPE: 1.44 MB storage  
COMPUTER: IBM 486 Compatible  
OPERATING SYSTEM: MS-DOS 5.0  
SOFTWARE: WordPerfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/494,301A  
FILING DATE: 23-JUNE-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9413035.8  
FILING DATE: 29-JUNE-1994  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleotide  
STRANDEDNESS: single  
TOPOLOGY: linear  
ANTI-SENSE: Yes  
US-08-494-301A-28

Query Match 30.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 9 ACGTGTACAG 18  
Db 11 ACAGGTACAG 2

## RESULT 58

US-08-777-266A-87/c  
Sequence 87, Application US/08/777266A  
Patent No. 6077833  
GENERAL INFORMATION:  
APPLICANT: Clarence Frank Bennett  
APPLICANT: Timothy A. Vickers  
TITLE OF INVENTION: Oligonucleotide Compositions and  
TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,266A  
FILING DATE: December 31, 1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 87:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-08-777-266A-87

Query Match 30.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 GTACGGGAG 22  
Db 12 GTACGGGAG 3

## RESULT 59

US-09-281-418-107/c  
Sequence 107, Application US/09281418  
Patent No. 8287769  
GENERAL INFORMATION:  
APPLICANT: Inoue, Takakazu  
TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA  
TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing M  
TITLE OF INVENTION: nisms and Method of Assaying Contaminant  
FILE REFERENCE: 9982-7  
CURRENT APPLICATION NUMBER: US/09/281,418

; CURRENT FILING DATE: 1999-03-30  
 ; EARLIER APPLICATION NUMBER: JP/1998/87651  
 ; EARLIER FILING DATE: 1998-03-31  
 ; EARLIER APPLICATION NUMBER: JP/1999/69694  
 ; EARLIER FILING DATE: 1999-03-16  
 ; NUMBER OF SEQ ID NOS: 216  
 ; SEQ ID NO 107  
 ; LENGTH: 12  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer  
 US-09-281-418-107

Query Match 30.0%; Score 8.4; DB 1; Length 12;  
 Best Local Similarity 90.0%; Pred. No. 51;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CTACGTGTAC 16  
 |||||  
 Db 12 CTTCGTGTAC 3

## RESULT 60

US-09-626-929-25  
 ; Sequence 25, Application US/09626929  
 ; Patent No. 6319714

; GENERAL INFORMATION:  
 ; APPLICANT: CRAMERI, ANDREAS  
 ; APPLICANT: STENMER, WILLEM P.C.  
 ; APPLICANT: MINSHULL, JEREMY  
 ; APPLICANT: BASS, STEVEN H.  
 ; APPLICANT: WELCH, MARK  
 ; APPLICANT: NESS, JON E.  
 ; APPLICANT: GUSTAFSSON, CLAES  
 ; APPLICANT: PATTEN, PHILIP A.  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION  
 ; FILE REFERENCE: 02-029620US  
 ; CURRENT APPLICATION NUMBER: US/09/626,929  
 2000-07-27

; CURRENT FILING DATE: 2000-07-27  
 ; PRIOR APPLICATION NUMBER: 09/408,392  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: 60/118,813  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: 60/141,049  
 ; PRIOR FILING DATE: 1999-06-24  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 25  
 ; LENGTH: 12  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(12)  
 US-09-626-929-25

Query Match 30.0%; Score 8.4; DB 1; Length 12;  
 Best Local Similarity 90.0%; Pred. No. 51;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27  
 |||||  
 Db 2 GGGGGTCCAG 11

## RESULT 61

US-09-326-186B-87/c  
 ; Sequence 87, Application US/09326186B  
 ; Patent No. 6319906  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bennett, Clarence Frank

; APPLICANT: Vickers, Timothy A.  
 ; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the  
 ; FILE REFERENCE: ISPH-0376  
 ; CURRENT APPLICATION NUMBER: US/09/326,186B  
 ; CURRENT FILING DATE: 1999-06-04  
 ; PRIOR APPLICATION NUMBER: 08/777,266  
 ; PRIOR FILING DATE: 1996-12-31  
 ; NUMBER OF SEQ ID NOS: 226  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 87  
 ; LENGTH: 12  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic  
 US-09-326-186B-87

Query Match 30.0%; Score 8.4; DB 1; Length 12;  
 Best Local Similarity 90.0%; Pred. No. 51;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GTACGGGAG 22  
 |||||  
 Db 12 GTACGGGAG 3

## RESULT 62

US-09-484-850-25  
 ; Sequence 25, Application US/09484850  
 ; Patent No. 6368861

; GENERAL INFORMATION:  
 ; APPLICANT: CRAMERI, ANDREAS  
 ; APPLICANT: STENMER, WILLEM P.C.  
 ; APPLICANT: MINSHULL, JEREMY  
 ; APPLICANT: BASS, STEVEN H.  
 ; APPLICANT: WELCH, MARK  
 ; APPLICANT: NESS, JON E.  
 ; APPLICANT: GUSTAFSSON, CLAES  
 ; APPLICANT: PATTEN, PHILIP A.  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION  
 ; FILE REFERENCE: 02-03630US  
 ; CURRENT APPLICATION NUMBER: US/09/484,850  
 ; CURRENT FILING DATE: 2000-01-18  
 ; PRIOR APPLICATION NUMBER: 09/408,392  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: 60/118,813  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: 60/141,049  
 ; PRIOR FILING DATE: 1999-06-24  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 25  
 ; LENGTH: 12  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(12)  
 US-09-484-850-25

Query Match 30.0%; Score 8.4; DB 1; Length 12;  
 Best Local Similarity 90.0%; Pred. No. 51;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27  
 |||||  
 Db 2 GGGGGTCCAG 11

## RESULT 63

US-09-408-392-25  
 ; Sequence 25, Application US/09408392

Patent No. 6376246  
; GENERAL INFORMATION:  
; APPLICANT: CRAMERI, ANDREAS  
; APPLICANT: STEMMER, WILLEM P.C.  
; APPLICANT: MINSHULL, JEREMY  
; APPLICANT: BASS, STEVEN H.  
; APPLICANT: WELCH, MARK  
; APPLICANT: NESS, JON E.  
; APPLICANT: GUSTAFSSON, CLAES  
; APPLICANT: PATTEN, PHILLIP A.  
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION  
; FILE REFERENCE: 02-0296200S  
; CURRENT APPLICATION NUMBER: US/09/408,392  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: 60/118,813  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: 60/141,049  
; PRIOR FILING DATE: 1999-06-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(12)  
US-09-408-392-25  
Query Match 30.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 18 GGGAGTCCAG 27  
Db 2 GGGGTCCAG 11  
RESULT 64  
US-09-626-930-25  
; Sequence 25, Application US/09626930  
; Patent No. 6423542  
; GENERAL INFORMATION:  
; APPLICANT: CRAMERI, ANDREAS  
; APPLICANT: STEMMER, WILLEM P.C.  
; APPLICANT: MINSHULL, JEREMY  
; APPLICANT: BASS, STEVEN H.  
; APPLICANT: WELCH, MARK  
; APPLICANT: NESS, JON E.  
; APPLICANT: GUSTAFSSON, CLAES  
; APPLICANT: PATTEN, PHILLIP A.  
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION  
; FILE REFERENCE: 02-0296200S  
; CURRENT APPLICATION NUMBER: US/09/408,392  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: 60/118,813  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: 60/141,049  
; PRIOR FILING DATE: 1999-06-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(12)  
US-09-626-930-25  
Query Match 30.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 18 GGGAGTCCAG 27  
Db 2 GGGGTCCAG 11  
RESULT 65  
US-09-626-528-25  
; Sequence 25, Application US/09626528  
; Patent No. 6426224  
; GENERAL INFORMATION:  
; APPLICANT: CRAMERI, ANDREAS  
; APPLICANT: STEMMER, WILLEM P.C.  
; APPLICANT: MINSHULL, JEREMY  
; APPLICANT: BASS, STEVEN H.  
; APPLICANT: WELCH, MARK  
; APPLICANT: NESS, JON E.  
; APPLICANT: GUSTAFSSON, CLAES  
; APPLICANT: PATTEN, PHILLIP A.  
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION  
; FILE REFERENCE: 02-0296200S  
; CURRENT APPLICATION NUMBER: US/09/408,392  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: 60/118,813  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: 60/141,049  
; PRIOR FILING DATE: 1999-06-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(12)  
US-09-626-528-25  
Query Match 30.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 18 GGGAGTCCAG 27  
Db 2 GGGGTCCAG 11  
RESULT 66  
US-09-340-861-39  
; Sequence 39, Application US/09340861  
; Patent No. 6432704  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 115  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)

Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 18 GGGAGTCCAG 27  
Db 2 GGGGTCCAG 11  
RESULT 65  
US-09-626-528-25  
; Sequence 25, Application US/09626528  
; Patent No. 6426224  
; GENERAL INFORMATION:  
; APPLICANT: CRAMERI, ANDREAS  
; APPLICANT: STEMMER, WILLEM P.C.  
; APPLICANT: MINSHULL, JEREMY  
; APPLICANT: BASS, STEVEN H.  
; APPLICANT: WELCH, MARK  
; APPLICANT: NESS, JON E.  
; APPLICANT: GUSTAFSSON, CLAES  
; APPLICANT: PATTEN, PHILLIP A.  
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION  
; FILE REFERENCE: 02-0296200S  
; CURRENT APPLICATION NUMBER: US/09/408,392  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: 60/118,813  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: 60/141,049  
; PRIOR FILING DATE: 1999-06-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(12)  
US-09-626-528-25  
Query Match 30.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 18 GGGAGTCCAG 27  
Db 2 GGGGTCCAG 11  
RESULT 66  
US-09-340-861-39  
; Sequence 39, Application US/09340861  
; Patent No. 6432704  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 115  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)



```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,861
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-340-861-39

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCCTACGTGT 14
DB 1 CCGGACGUGU 10

RESULT 67
US-09-634-262-39
; Sequence 39, Application US/09634262
; Patent No. 6440719
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/634,262
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209

```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-634-262-39

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCCTACGTGT 14
DB 1 CCGGACGUGU 10

RESULT 68
US-09-626-595-25
; Sequence 25, Application US/09626595
; Patent No. 6479652
; GENERAL INFORMATION:
; APPLICANT: CRAMERI, ANDREAS
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: BASS, STEVEN H.
; APPLICANT: WELCH, MARK
; APPLICANT: NESS, JON E.
; APPLICANT: GUSTAFSSON, CLAES
; APPLICANT: PATTEN, PHILLIP A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
; FILE REFERENCE: 02-029620US
; CURRENT APPLICATION NUMBER: US/09/626,595
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/408,392
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/118,813
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/141,049
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(12)
; US-09-626-595-25

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27
DB 2 GGGGTCAG 11

RESULT 69
US-09-694-863-25
; Sequence 25, Application US/09694863
; Patent No. 6521453
; GENERAL INFORMATION:
; APPLICANT: CRAMERI, ANDREAS
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: BASS, STEVEN H.

```

APPLICANT: WELCH, MARK  
APPLICANT: NESS, JON E.  
APPLICANT: GUSTAFSSON, CLAES  
APPLICANT: PATTEN, PHILIP A.  
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION  
FILE REFERENCE: 02-029620US  
CURRENT APPLICATION NUMBER: US/09/694,863  
CURRENT FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 09/408,392  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: 60/141,049  
PRIOR FILING DATE: 1999-06-24  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 25  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(12)  
US-09-694-863-25

Query Match 30.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GGGAGTCCAG 27  
Db 2 GGGGTCCAG 11

RESULT 70  
US-08-702-665A-19/c  
Sequence 19, Application US/08702665A  
Patent No. 6274708  
GENERAL INFORMATION:  
APPLICANT: HILTON, Douglas J.  
TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States of America  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,665A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Presser, Leopold  
REGISTRATION NUMBER: 19,827  
REFERENCE/DOCKET NUMBER: 10296  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 203 901 SANS UR  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-702-665A-19

Query Match 29.3%; Score 8.2; DB 1; Length 21;  
Best Local Similarity 76.9%; Pred. No. 1.3e+02;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CTACGTTACAGG 19  
Db 15 CTCCAAGTACAGG 3

RESULT 71  
US-09-989-789-2098/c  
Sequence 2098, Application US/09989789  
Patent No. 6586746  
GENERAL INFORMATION:  
APPLICANT: LIU, Qiang  
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
FILE REFERENCE: 8325-0011.20 / S11-US2  
CURRENT APPLICATION NUMBER: US/09/989,789  
CURRENT FILING DATE: 2002-03-25  
NUMBER OF SEQ ID NOS: 4085  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2098  
LENGTH: 9  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: example target  
OTHER INFORMATION: DNA  
US-09-989-789-2098

Query Match 28.6%; Score 8; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCTTACGT 12  
Db 9 CCTTACGT 2

RESULT 72  
US-09-989-789-2100/c  
Sequence 2100, Application US/09989789  
Patent No. 6586746  
GENERAL INFORMATION:  
APPLICANT: LIU, Qiang  
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
FILE REFERENCE: 8325-0011.20 / S11-US2  
CURRENT APPLICATION NUMBER: US/09/989,789  
CURRENT FILING DATE: 2002-03-25  
NUMBER OF SEQ ID NOS: 4085  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2100  
LENGTH: 9  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: example target  
OTHER INFORMATION: DNA  
US-09-989-789-2100

Query Match 28.6%; Score 8; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCTTACGT 12  
Db 9 CCTTACGT 2

RESULT 73  
US-09-989-789-2195

; Sequence 2195, Application US/09989789  
; Patent No. 6588746  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2195  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-2195

Query Match 28.6%; Score 8; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 AGGGAGTC 24  
| | | | | | | | | |  
Db 2 AGGGAGTC 9

RESULT 74  
US-09-989-789-2453/c  
; Sequence 2453, Application US/09989789  
; Patent No. 6588746  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2453  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-2453

Query Match 28.6%; Score 8; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8  
| | | | | | | | | |  
Db 9 CGGGCCCT 2

RESULT 75  
US-09-989-789-2454/c  
; Sequence 2454, Application US/09989789  
; Patent No. 6588746  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2454  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-2454

Query Match 28.6%; Score 8; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8  
| | | | | | | | | |  
Db 9 CGGGCCCT 2

RESULT 76  
US-08-170-095B-12  
; Sequence 12, Application US/08170095B  
; Patent No. 5563254  
; GENERAL INFORMATION:  
; APPLICANT: Hoffman, Stephen J.  
; APPLICANT: Nagai, Kiyoshi  
; TITLE OF INVENTION: Blood Substitutes  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Somatogen, Inc.  
; STREET: 2545 Central Avenue  
; CITY: Boulder  
; STATE: Colorado  
; ZIP: 80301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: System 7.0.1  
; SOFTWARE: Microsoft Word 5.0a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/170,095B  
; FILING DATE: December 20, 1993  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5563254ak, Henry P.  
; REGISTRATION NUMBER: 33200  
; REFERENCE/DOCKET NUMBER: Hoffman 2A/CONT2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 303-541-3322  
; TELEFAX: 303-444-3013  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown to applicant  
; MOLECULE TYPE: Other nucleic acid  
; DESCRIPTION: ARTIFICIALLY GENERATED OLIGONUCLEOTIDE USED IN A CL  
; HYPOTHETICAL: no  
US-08-170-095B-12

Query Match 28.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8  
| | | | | | | | | |  
Db 3 CGGGCCCT 10

RESULT 77  
US-08-396-866-12  
; Sequence 12, Application US/08396866  
; Patent No. 5661124

Query Match	28.6%	Score 8	DB 1	Length 10
Best Local Similarity	100.0%	Pred. No. 45		
Matches	8	Conservative 0	Mismatches 0	Indels 0
Gaps	0			
QY	17	AGGGAGTC 24		
DB	9	AGGGAGTC 2		
RESULT 79				
US-09-193-707-9				
Sequence 9		Application US/09193707		
Patent No. 6524792				
GENERAL INFORMATION:				
APPLICANT: Renner, Wolfgang A.				
APPLICANT: Orberger, Georg H.				
APPLICANT: Koller, Daniel				
APPLICANT: Bailey, James E.				
TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE DISCOVERY				
TITLE OF INVENTION: CHARACTERIZATION AND ISOLATION OF GENES ENCODING POLYPEPTIDES WI				
FILE REFERENCE: 8358-0005-999				
CURRENT APPLICATION NUMBER: US/09/193,707				
CURRENT FILING DATE: 1998-11-17				
NUMBER OF SEQ ID NOS: 18				
SOFTWARE: FastSeq for Windows Version 3.0				
SEQ ID NO 9				
LENGTH: 11				
TYPE: DNA				
ORGANISM: Artificial Sequence				
FEATURE:				
OTHER INFORMATION: Primer				
US-09-193-707-9				
Query Match	28.6%	Score 8	DB 1	Length 11
Best Local Similarity	100.0%	Pred. No. 55		
Matches	8	Conservative 0	Mismatches 0	Indels 0
Gaps	0			
QY	1	CGGGCCCT 8		
DB	4	CGGGCCCT 11		
RESULT 80				
US-08-086-410-4				
Sequence 4		Application US/08086410		
Patent No. 5407822				
GENERAL INFORMATION:				
APPLICANT: LEPLATOIS, Pascal				
APPLICANT: LOISON, Gerard				
APPLICANT: PESSEQUE, Bernard				
APPLICANT: SHIRE, David				
TITLE OF INVENTION: Artificial promoter for the expression				
TITLE OF INVENTION: of proteins in yeast				
NUMBER OF SEQUENCES: 37				
CORRESPONDENCE ADDRESS:				
ADDRESSEE: FOLEY & LARDNER				
STREET: King Street Station, Suite 500, 1800 Diagonal				
STREET: Road, PO Box 299				
CITY: ALEXANDRIA				
STATE: VIRGINIA				
COUNTRY: USA				
ZIP: 22313-0299				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Floppy disk				
COMPUTER: IBM PC compatible				
OPERATING SYSTEM: PC-DOS/MS-DOS				
SOFTWARE: Patent in Release #1.0, Version #1.25				
CURRENT APPLICATION DATA:				
APPLICATION NUMBER: US/08/086,410				
FILING DATE:				

Query Match	28.6%	Score 8	DB 1	Length 10
Best Local Similarity	100.0%	Pred. No. 45		
Matches	8	Conservative 0	Mismatches 0	Indels 0
QY	17	AGGGAGTC 24		
DB	9	AGGGAGTC 2		
<p>US-09-301-721A-12</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Hoffman, Stephen J.</p> <p>TITLE OF INVENTION: Blood Substitutes</p> <p>NUMBER OF SEQUENCES: 34</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Somatogen, Inc.</p> <p>STREET: 5797 Central Avenue</p> <p>CITY: Boulder</p> <p>STATE: Colorado</p> <p>ZIP: 80301</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage</p> <p>COMPUTER: Apple Macintosh</p> <p>OPERATING SYSTEM: System 7.0.1</p> <p>SOFTWARE: Microsoft Word 5.0a</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/396,866</p> <p>FILING DATE:</p> <p>CLASSIFICATION: 530</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/062,780</p> <p>FILING DATE: May 17, 1993</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: No. 566112ak, Henry P.</p> <p>REGISTRATION NUMBER: 33200</p> <p>REFERENCE/DOCKET NUMBER: Hoffman</p> <p>REFERENCE/DOCKET NUMBER: 2A/CONT1</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 303-541-3322</p> <p>TELEFAX: 303-444-3013</p> <p>INFORMATION FOR SEQ ID NO: 12:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 10</p> <p>TYPE: nucleic acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: unknown to applicant</p> <p>MOLECULE TYPE: Other nucleic acid</p> <p>DESCRIPTION: ARTIFICIALLY GENERATED OLIGONUCLEOTIDE</p> <p>DESCRIPTION: USED IN A CLONING VECTOR</p> <p>HYPOTHETICAL: no</p> <p>US-08-396-866-12</p>				
QY	1	CGGGCCCT 8		
DB	3	CGGGCCCT 10		
<p>Query Match 28.6%; Score 8; DB 1; Length 10;</p> <p>Best Local Similarity 100.0%; Pred. No. 45;</p> <p>Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>				
<p>US-09-301-721A-12/c</p> <p>Sequence 12, Application US/09301721A</p> <p>Patent No. 6506561</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: CHEVAL, Lydie</p> <p>APPLICANT: ELALOUF, Jean-Marc</p> <p>APPLICANT: VILON, Berangere</p> <p>TITLE OF INVENTION: MICROASSAY FOR SERIAL ANALYSIS OF GENE EXPRESSION AND</p> <p>TITLE OF INVENTION: APPLICATIONS THEREOF</p> <p>FILE REFERENCE: 0846-0499-0X</p> <p>CURRENT APPLICATION NUMBER: US/09/301,721A</p> <p>CURRENT FILING DATE: 1999-04-29</p> <p>PRIOR APPLICATION NUMBER: EPO 99400189.9</p> <p>PRIOR FILING DATE: 1999-01-27</p> <p>NUMBER OF SEQ ID NOS: 28</p> <p>SOFTWARE: Patent in Ver. 2.1</p> <p>SEQ ID NO 12</p> <p>LENGTH: 10</p> <p>TYPE: DNA</p> <p>ORGANISM: Mus musculus</p>				
QY	1	CGGGCCCT 8		
DB	3	CGGGCCCT 10		
<p>Query Match 28.6%; Score 8; DB 1; Length 10;</p> <p>Best Local Similarity 100.0%; Pred. No. 45;</p> <p>Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>				
<p>US-09-301-721A-12</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Hoffman, Stephen J.</p> <p>TITLE OF INVENTION: Blood Substitutes</p> <p>NUMBER OF SEQUENCES: 34</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Somatogen, Inc.</p> <p>STREET: 5797 Central Avenue</p> <p>CITY: Boulder</p> <p>STATE: Colorado</p> <p>ZIP: 80301</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage</p> <p>COMPUTER: Apple Macintosh</p> <p>OPERATING SYSTEM: System 7.0.1</p> <p>SOFTWARE: Microsoft Word 5.0a</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/396,866</p> <p>FILING DATE:</p> <p>CLASSIFICATION: 530</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/062,780</p> <p>FILING DATE: May 17, 1993</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: No. 566112ak, Henry P.</p> <p>REGISTRATION NUMBER: 33200</p> <p>REFERENCE/DOCKET NUMBER: Hoffman</p> <p>REFERENCE/DOCKET NUMBER: 2A/CONT1</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 303-541-3322</p> <p>TELEFAX: 303-444-3013</p> <p>INFORMATION FOR SEQ ID NO: 12:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 10</p> <p>TYPE: nucleic acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: unknown to applicant</p> <p>MOLECULE TYPE: Other nucleic acid</p> <p>DESCRIPTION: ARTIFICIALLY GENERATED OLIGONUCLEOTIDE</p> <p>DESCRIPTION: USED IN A CLONING VECTOR</p> <p>HYPOTHETICAL: no</p> <p>US-08-396-866-12</p>				
QY	1	CGGGCCCT 8		
DB	3	CGGGCCCT 10		
<p>Query Match 28.6%; Score 8; DB 1; Length 10;</p> <p>Best Local Similarity 100.0%; Pred. No. 45;</p> <p>Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>				
<p>US-09-301-721A-12</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Hoffman, Stephen J.</p> <p>TITLE OF INVENTION: Blood Substitutes</p> <p>NUMBER OF SEQUENCES: 34</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Somatogen, Inc.</p> <p>STREET: 5797 Central Avenue</p> <p>CITY: Boulder</p> <p>STATE: Colorado</p> <p>ZIP: 80301</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage</p> <p>COMPUTER: Apple Macintosh</p> <p>OPERATING SYSTEM: System 7.0.1</p> <p>SOFTWARE: Microsoft Word 5.0a</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/396,866</p> <p>FILING DATE:</p> <p>CLASSIFICATION: 530</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/062,780</p> <p>FILING DATE: May 17, 1993</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: No. 566112ak, Henry P.</p> <p>REGISTRATION NUMBER: 33200</p> <p>REFERENCE/DOCKET NUMBER: Hoffman</p> <p>REFERENCE/DOCKET NUMBER: 2A/CONT1</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 303-541-3322</p> <p>TELEFAX: 303-444-3013</p> <p>INFORMATION FOR SEQ ID NO: 12:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 10</p> <p>TYPE: nucleic acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: unknown to applicant</p> <p>MOLECULE TYPE: Other nucleic acid</p> <p>DESCRIPTION: ARTIFICIALLY GENERATED OLIGONUCLEOTIDE</p> <p>DESCRIPTION: USED IN A CLONING VECTOR</p> <p>HYPOTHETICAL: no</p> <p>US-08-396-866-12</p>				
QY	1	CGGGCCCT 8		
DB	3	CGGGCCCT 10		
<p>Query Match 28.6%; Score 8; DB 1; Length 10;</p> <p>Best Local Similarity 100.0%; Pred. No. 45;</p> <p>Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>				
<p>US-09-301-721A-12</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Hoffman, Stephen J.</p> <p>TITLE OF INVENTION: Blood Substitutes</p> <p>NUMBER OF SEQUENCES: 34</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Somatogen, Inc.</p> <p>STREET: 5797 Central Avenue</p> <p>CITY: Boulder</p> <p>STATE: Colorado</p> <p>ZIP: 80301</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage</p> <p>COMPUTER: Apple Macintosh</p> <p>OPERATING SYSTEM: System 7.0.1</p> <p>SOFTWARE: Microsoft Word 5.0a</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/396,866</p> <p>FILING DATE:</p> <p>CLASSIFICATION: 530</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/062,780</p> <p>FILING DATE: May 17, 1993</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: No. 566112ak, Henry P.</p> <p>REGISTRATION NUMBER: 33200</p> <p>REFERENCE/DOCKET NUMBER: Hoffman</p> <p>REFERENCE/DOCKET NUMBER: 2A/CONT1</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 303-541-3322</p> <p>TELEFAX: 303-444-3013</p> <p>INFORMATION FOR SEQ ID NO: 12:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 10</p> <p>TYPE: nucleic acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: unknown to applicant</p> <p>MOLECULE TYPE: Other nucleic acid</p> <p>DESCRIPTION: ARTIFICIALLY GENERATED OLIGONUCLEOTIDE</p> <p>DESCRIPTION: USED IN A CLONING VECTOR</p> <p>HYPOTHETICAL: no</p> <p>US-08-396-866-12</p>				
QY	1	CGGGCCCT 8		
DB	3	CGGGCCCT 10		
<p>Query Match 28.6%; Score 8; DB 1; Length 10;</p> <p>Best Local Similarity 100.0%; Pred. No. 45;</p> <p>Matches 8; Conservative 0;</p>				

Query Match	28.6%	Score 8	DB 1	Length 10
Best Local Similarity	100.0%	Pred. No. 45		
Matches	8	Conservative 0	Mismatches 0	Indels 0
QY	17	AGGGAGTC 24		
DB	9	AGGGAGTC 2		
<p>US-09-301-721A-12</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Hoffman, Stephen J.</p> <p>TITLE OF INVENTION: Blood Substitutes</p> <p>NUMBER OF SEQUENCES: 34</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Somatogen, Inc.</p> <p>STREET: 5797 Central Avenue</p> <p>CITY: Boulder</p> <p>STATE: Colorado</p> <p>ZIP: 80301</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage</p> <p>COMPUTER: Apple Macintosh</p> <p>OPERATING SYSTEM: System 7.0.1</p> <p>SOFTWARE: Microsoft Word 5.0a</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/396,866</p> <p>FILING DATE:</p> <p>CLASSIFICATION: 530</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/062,780</p> <p>FILING DATE: May 17, 1993</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: No. 566112ak, Henry P.</p> <p>REGISTRATION NUMBER: 33200</p> <p>REFERENCE/DOCKET NUMBER: Hoffman</p> <p>REFERENCE/DOCKET NUMBER: 2A/CONT1</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 303-541-3322</p> <p>TELEFAX: 303-444-3013</p> <p>INFORMATION FOR SEQ ID NO: 12:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 10</p> <p>TYPE: nucleic acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: unknown to applicant</p> <p>MOLECULE TYPE: Other nucleic acid</p> <p>DESCRIPTION: ARTIFICIALLY GENERATED OLIGONUCLEOTIDE</p> <p>DESCRIPTION: USED IN A CLONING VECTOR</p> <p>HYPOTHETICAL: no</p> <p>US-08-396-866-12</p>				
QY	1	CGGGCCCT 8		
DB	3	CGGGCCCT 10		
<p>Query Match 28.6%; Score 8; DB 1; Length 10;</p> <p>Best Local Similarity 100.0%; Pred. No. 45;</p> <p>Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>				
<p>US-09-301-721A-12/c</p> <p>Sequence 12, Application US/09301721A</p> <p>Patent No. 6506561</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: CHEVAL, Lydie</p> <p>APPLICANT: ELALOUF, Jean-Marc</p> <p>APPLICANT: VILON, Berangere</p> <p>TITLE OF INVENTION: MICROASSAY FOR SERIAL ANALYSIS OF GENE EXPRESSION AND</p> <p>TITLE OF INVENTION: APPLICATIONS THEREOF</p> <p>FILE REFERENCE: 0846-0499-0X</p> <p>CURRENT APPLICATION NUMBER: US/09/301,721A</p> <p>CURRENT FILING DATE: 1999-04-29</p> <p>PRIOR APPLICATION NUMBER: EPO 99400189.9</p> <p>PRIOR FILING DATE: 1999-01-27</p> <p>NUMBER OF SEQ ID NOS: 28</p> <p>SOFTWARE: Patent in Ver. 2.1</p> <p>SEQ ID NO 12</p> <p>LENGTH: 10</p> <p>TYPE: DNA</p> <p>ORGANISM: Mus musculus</p>				
QY	1	CGGGCCCT 8		
DB	3	CGGGCCCT 10		
<p>Query Match 28.6%; Score 8; DB 1; Length 10;</p> <p>Best Local Similarity 100.0%; Pred. No. 45;</p> <p>Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>				
<p>US-08-086-410-4</p> <p>Sequence 4, Application US/08086410</p> <p>Patent No. 5407822</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: LEPLATOIS, Pascal</p> <p>APPLICANT: LOISON, Gerard</p> <p>APPLICANT: PESSEQUE, Bernard</p> <p>APPLICANT: SHIRE, David</p> <p>TITLE OF INVENTION: Artificial promoter for the expression</p> <p>TITLE OF INVENTION: of proteins in yeast</p> <p>NUMBER OF SEQUENCES: 37</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: FOLEY &amp; LARDNER</p> <p>STREET: King Street Station, Suite 500, 1800 Diagonal</p> <p>STREET: Road, PO Box 299</p> <p>CITY: ALEXANDRIA</p> <p>STATE: VIRGINIA</p> <p>COUNTRY: USA</p> <p>ZIP: 22313-0299</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent in Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/086,410</p> <p>FILING DATE:</p>				
QY	1	CGGGCCCT 8		
DB	4	CGGGCCCT 11		
<p>Query Match 28.6%; Score 8; DB 1; Length 11;</p> <p>Best Local Similarity 100.0%; Pred. No. 55;</p> <p>Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>				
<p>US-09-193-707-9</p> <p>Sequence 9, Application US/09193707</p> <p>Patent No. 6524792</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Renner, Wolfgang A.</p> <p>APPLICANT: Orberger, Georg H.</p> <p>APPLICANT: Koller, Daniel</p> <p>APPLICANT: Bailey, James E.</p> <p>TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE DISCOVERY</p> <p>TITLE OF INVENTION: CHARACTERIZATION AND ISOLATION OF GENES ENCODING POLYPEPTIDES WI</p> <p>FILE REFERENCE: 8358-0005-999</p> <p>CURRENT APPLICATION NUMBER: US/09/193,707</p> <p>CURRENT FILING DATE: 1998-11-17</p> <p>NUMBER OF SEQ ID NOS: 18</p> <p>SOFTWARE: FastSeq for Windows Version 3.0</p> <p>SEQ ID NO 9</p> <p>LENGTH: 11</p> <p>TYPE: DNA</p> <p>ORGANISM: Artificial Sequence</p> <p>FEATURE:</p> <p>OTHER INFORMATION: Primer</p> <p>US-09-193-707-9</p>				
QY	1	CGGGCCCT 8		
DB	4	CGGGCCCT 11		
<p>Query Match 28.6%; Score 8; DB 1; Length 11;</p> <p>Best Local Similarity 100.0%; Pred. No. 55;</p> <p>Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>				
<p>US-08-086-410-4</p> <p>Sequence 4, Application US/08086410</p> <p>Patent No. 5407822</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: LEPLATOIS, Pascal</p> <p>APPLICANT: LOISON, Gerard</p> <p>APPLICANT: PESSEQUE, Bernard</p> <p>APPLICANT: SHIRE, David</p> <p>TITLE OF INVENTION: Artificial promoter for the expression</p> <p>TITLE OF INVENTION: of proteins in yeast</p> <p>NUMBER OF SEQUENCES: 37</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: FOLEY &amp; LARDNER</p> <p>STREET: King Street Station, Suite 500, 1800 Diagonal</p> <p>STREET: Road, PO Box 299</p> <p>CITY: ALEXANDRIA</p> <p>STATE: VIRGINIA</p> <p>COUNTRY: USA</p> <p>ZIP: 22313-0299</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent in Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/086,410</p> <p>FILING DATE:</p>				

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,083  
FILING DATE: 02-OCT-1991  
APPLICATION NUMBER: FR 89 17467  
FILING DATE: 29-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Saxe, Bernhard D  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 16781/318  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 836-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
IMMEDIATE SOURCE:  
CLONE: oligonucleotide/primer of reverse  
US-08-086-410-4

Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8  
Db 5 CGGGCCCT 12

RESULT 81  
US-07-939-501A-17  
Sequence 17, Application US/07939501A  
Patent No. 5446138  
GENERAL INFORMATION:  
APPLICANT: BLAISEAU, Pierre-Louis  
APPLICANT: LEGOUX, Richard  
APPLICANT: LEGUAY, Jean-Jacques  
APPLICANT: SCHNEIDER, Michel  
TITLE OF INVENTION: Recombinant DNA coding for a protein  
TITLE OF INVENTION: having endochitinase activity  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: King Street Station, Suite 500, 1800 Diagonal  
CITY: ALEXANDRIA  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/939,501A  
FILING DATE: 19920908  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 11072  
FILING DATE: 06-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Saxe, Bernhard D  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 16781/373  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-9300

TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-07-939-501A-17

Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8  
Db 5 CGGGCCCT 12

RESULT 82  
US-08-025-038-15/c  
Sequence 15, Application US/08025038  
Patent No. 5545526  
GENERAL INFORMATION:  
APPLICANT: BAXTER-LOWE, Lee-Ann  
TITLE OF INVENTION: Method For HLA Typing  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 777 E. Wisconsin Avenue  
CITY: Milwaukee  
STATE: Wisconsin  
COUNTRY: USA  
ZIP: 53202-5367  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/025,038  
FILING DATE: 19930301  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/544,218  
FILING DATE: 27-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Philip G.  
REGISTRATION NUMBER: 30,478  
REFERENCE/DOCKET NUMBER: 204 854  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (414)289-3761  
TELEFAX: (414)289-3791  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-025-038-15

Query Match 28.6%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8  
Db 9 CGGGCCCT 2

RESULT 83  
US-08-152-955-4

; Sequence 4, Application US/08152955  
; Patent No. 5474897  
; GENERAL INFORMATION:  
; APPLICANT: Weiss, Arthur  
; TITLE OF INVENTION: Screening Assay for the Identification  
; TITLE OF INVENTION: Screening Assay for the Identification  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/152,955  
; CLASSIFICATION: 435  
; APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: US 07/898,639  
; FILING DATE: 15-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heslin, James M.  
; REGISTRATION NUMBER: 29,541  
; REFERENCE/POCKET NUMBER: 2307U-356  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-152-955-4

Query Match 27.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 63;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 CAGGAGTCCA 26  
Db 1 CAGAGATCCA 11

RESULT 84  
US-09-249-155A-236  
; Sequence 236, Application US/09249155A  
; Patent No. 6538173  
; GENERAL INFORMATION:  
; APPLICANT: Heber-Katz, Ellen  
; TITLE OF INVENTION: Compositions and Methods for Wound  
; TITLE OF INVENTION: Healing  
; FILE REFERENCE: 00486.78503  
; CURRENT APPLICATION NUMBER: US/09/249,155A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/097,937  
; PRIOR FILING DATE: 1998-08-26  
; PRIOR APPLICATION NUMBER: US 60/102,051  
; NUMBER OF SEQ ID NOS: 346  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 236  
; LENGTH: 11  
; TYPE: DNA

; ORGANISM: Mus musculus  
US-09-249-155A-236  
Query Match 27.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 63;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 GGGAGTCCAGG 28  
Db 1 GGGGGCCAGG 11

RESULT 85  
US-09-249-155A-272/C  
; Sequence 272, Application US/09249155A  
; Patent No. 6538173  
; GENERAL INFORMATION:  
; APPLICANT: Heber-Katz, Ellen  
; TITLE OF INVENTION: Compositions and Methods for Wound  
; TITLE OF INVENTION: Healing  
; FILE REFERENCE: 00486.78503  
; CURRENT APPLICATION NUMBER: US/09/249,155A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/097,937  
; PRIOR FILING DATE: 1998-08-26  
; PRIOR APPLICATION NUMBER: US 60/102,051  
; PRIOR FILING DATE: 1998-09-28  
; NUMBER OF SEQ ID NOS: 346  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 272  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-249-155A-272

Query Match 27.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 63;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGTGTACAGG 20  
Db 11 CTTGTACAGG 1

RESULT 86  
PCT-US93-05668-4  
; Sequence 4, Application PC/TUS9305668  
; GENERAL INFORMATION:  
; APPLICANT: Weiss, Arthur  
; APPLICANT: Fraser, James  
; TITLE OF INVENTION: Screening Assay for the Identification  
; TITLE OF INVENTION: of Immunosuppressive Drugs  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fisher & Amzel  
; STREET: 1320 Harbor Bay Parkway, Suite 225  
; CITY: Alameda  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94501  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/05668  
; FILING DATE: 19930611  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/898,639

FILING DATE: 15-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fisher, Stanley P.  
REGISTRATION NUMBER: 24,344  
REFERENCE/DOCKET NUMBER: 81-143-1PCT  
TELEPHONE: 510-748-6868  
TELEFAX: 510-748-6688  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US93-05668-4

Query Match 27.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 63;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 16 CAGGAGTCCA 26  
DB 1 CAGAGATTCCA 11

RESULT 87  
US-08-035-928-19/c  
Sequence 19, Application US/08035928  
Patent No. 5538844  
GENERAL INFORMATION:  
APPLICANT: Duyao, Mabel P.  
APPLICANT: MacDonald, Marcy E.  
APPLICANT: Gusella, James F.  
TITLE OF INVENTION: A No. 5538844el Transport Protein Gene from the Huntington's Disease Region  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1225 Connecticut Avenue N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/035,928  
FILING DATE: 19930323  
CLASSIFICATION: 435  
TELEPHONE: (202) 466-0800  
TELEFAX: (202) 833-8716  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: both  
TOPOLOGY: linear  
US-08-035-928-19

Query Match 27.9%; Score 7.8; DB 1; Length 12;  
Best Local Similarity 81.8%; Pred. No. 74;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 CCCTACGTGTA 15  
DB 12 CCCTACGTGAA 2

RESULT 88  
US-08-435-350-107/c  
Sequence 107, Application US/08435350  
Patent No. 5599704  
GENERAL INFORMATION:  
APPLICANT: James D. Thompson  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TREATMENT OF BREAST CANCER  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,350  
FILING DATE: 05-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/936,531  
FILING DATE: August 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 197/245  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 107:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-435-350-107

Query Match 27.9%; Score 7.8; DB 1; Length 12;  
Best Local Similarity 81.8%; Pred. No. 74;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 GCCTACGTGT 14  
DB 12 GCCGTAGTGT 2  
RESULT 89  
US-08-494-301A-25/c  
Sequence 25, Application US/08494301A  
Patent No. 5856461  
GENERAL INFORMATION:  
APPLICANT: Colote, Soudhir  
APPLICANT: Pirotzky, Eduardo  
TITLE OF INVENTION: Oligonucleotides to Inhibit the  
Expression of Isoprenyl Protein Transferases  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lucas & Just  
STREET: 205 E. 42nd Street  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10017  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch,  
MEDIUM TYPE: 1.44 MB storage  
COMPUTER: IBM 486 Compatible  
OPERATING SYSTEM: MS-DOS 5.0  
SOFTWARE: WordPerfect 5.0  
CURRENT APPLICATION NUMBER: US/08/494,301A  
FILING DATE: 23-JUNE-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9413035.8  
FILING DATE: 29-JUNE-1994  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleotide  
STRANDEDNESS: single  
TOPOLOGY: linear  
ANTI-SENSE: Yes  
US-08-494-301A-25

Query Match 27.9%; Score 7.8; DB 1; Length 12;  
Best Local Similarity 81.8%; Pred. No. 74;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGAGT 23  
DB 11 GTCCAGAGT 1

## RESULT 90

US-09-281-418-25/c  
Sequence 25, Application US/09281418  
Patent No. 6287769  
GENERAL INFORMATION:  
APPLICANT: Inoue, Takakazu  
TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F  
TITLE OF INVENTION: agent, Method of Assaying Microorganisms, Method of Analyzing Mi  
TITLE OF INVENTION: nisms and Method of Assaying Contaminant  
FILE REFERENCE: 9982-7  
CURRENT APPLICATION NUMBER: US/09/281.418  
CURRENT FILING DATE: 1999-03-30  
EARLIER APPLICATION NUMBER: JP/1998/87651  
EARLIER FILING DATE: 1998-03-31  
EARLIER APPLICATION NUMBER: JP/1999/69694  
EARLIER FILING DATE: 1999-03-16  
NUMBER OF SEQ ID NOS: 216  
SEQ ID NO 25  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
US-09-281-418-25

Query Match 27.9%; Score 7.8; DB 1; Length 12;  
Best Local Similarity 81.8%; Pred. No. 74;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTACGTGTACA 17  
DB 11 CTTCGTGTAGA 1

## RESULT 91

US-09-528-404-9  
Sequence 9, Application US/09528404  
Patent No. 6440723  
GENERAL INFORMATION:  
APPLICANT: Roderic M.K. Dale  
TITLE OF INVENTION: ARRAYS WITH MODIFIED OLIGONUCLEOTIDE AND  
TITLE OF INVENTION: POLYNUCLEOTIDE COMPOSITIONS  
FILE REFERENCE: OLIG-002CIP3

CURRENT APPLICATION NUMBER: US/09/528,404  
CURRENT FILING DATE: 2000-03-17  
EARLIER APPLICATION NUMBER: 09/223,498  
EARLIER FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: 09/408,088  
EARLIER FILING DATE: 1999-09-29  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 12  
TYPE: RNA  
ORGANISM: rat  
US-09-528-404-9

Query Match 27.9%; Score 7.8; DB 1; Length 12;  
Best Local Similarity 72.7%; Pred. No. 74;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCC 25  
DB 1 AUAGGGAUCC 11

## RESULT 92

US-08-717-526-61/c  
Sequence 61, Application US/08717526  
Patent No. 5786147  
GENERAL INFORMATION:  
APPLICANT: MABILAT, CLAUDE  
APPLICANT: RAULT, DIDIER  
TITLE OF INVENTION: DETECTION OF ENTEROBACTERIA  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OLIFF & BERRIDGE  
STREET: 700 SOUTH WASHINGTON STREET  
CITY: ALEXANDRIA  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/717,526  
FILING DATE: 17-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BERRIDGE, WILLIAM P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 38732  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-717-526-61

Query Match 26.4%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.1e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGT 23  
DB 9 ACAGAGAT 1



```

RESULT 93
US-09-153-242-30
; Sequence 30, Application US/09153242
; Patent No. 6482592
; GENERAL INFORMATION:
; APPLICANT: Lundberg, Joakim
; APPLICANT: Uhlen, Mathias
; TITLE OF INVENTION: MODULAR PROBES II
; FILE REFERENCE: 1181-242
; CURRENT APPLICATION NUMBER: US/09/153,242
; CURRENT FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/GB97/02629
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide H1-9
US-09-153-242-30

Query Match      26.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGGCCCTAC 10
Db      1 GGGCCCTCC 9

RESULT 94
US-07-651-710A-33/c
; Sequence 33, Application US/07651710A
; Patent No. 5362864
; GENERAL INFORMATION:
; APPLICANT: Chua, Nam-Hai
; TITLE OF INVENTION: Trans-Activating Factor-1
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/651,710A
; FILING DATE: 19910206
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3288-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 8698864/9741
; TELEFAX: 66141 PENNIE
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: TAF-1 binding motif
US-07-651-710A-33

Query Match      26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 CTACGTGTA 15
Db      9 CCACGTGTA 1

RESULT 95
US-07-651-710A-38/c
; Sequence 38, Application US/07651710A
; Patent No. 5362864
; GENERAL INFORMATION:
; APPLICANT: Chua, Nam-Hai
; TITLE OF INVENTION: Trans-Activating Factor-1
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/651,710A
; FILING DATE: 19910206
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3288-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 66141 PENNIE
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: TAF-1 binding motif
US-07-651-710A-38

Query Match      26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 CTACGTGTA 15
Db      9 CCACGTGTA 1

RESULT 96
US-08-074-879-3
; Sequence 3, Application US/08074879
; Patent No. 5656423
; GENERAL INFORMATION:
; APPLICANT: Orth, Gerard
; APPLICANT: Volpers, Christoph
; APPLICANT: Streek, Rolf
; TITLE OF INVENTION: DNA Sequences Derived from the Genome of
; TITLE OF INVENTION: the Papillomavirus HPV39, Their Use in In Vitro Diagnosis
; TITLE OF INVENTION: and for the Production of an Immunogenic Composition
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/074,879  
FILING DATE: 16-JUN-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 92/1136  
FILING DATE: 09-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E.R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 02356.0066-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-074-879-3

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGT 23  
DB 1 AAAGGGAGT 9

RESULT 97  
US-08-468-057A-3  
Sequence 3, Application US/08468057A  
Patent No. 568535  
GENERAL INFORMATION:  
APPLICANT: Orth, Gerard  
APPLICANT: Volpers, Christoph  
APPLICANT: Streek, Rolf  
TITLE OF INVENTION: DNA Sequences Derived from the Genome of  
TITLE OF INVENTION: the Papillomavirus HPV39, Their Use in In Vitro Diagnosis  
TITLE OF INVENTION: and for the Production of an Immunogenic Composition  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,057A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/074,879  
FILING DATE: 16-JUN-1993  
APPLICATION NUMBER: WO 92/1136  
FILING DATE: 09-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E.R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 02356.0066-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-468-057A-3

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGT 23  
DB 1 AAAGGGAGT 9

RESULT 98  
US-08-378-986-6  
Sequence 6, Application US/08378986  
Patent No. 5723751  
GENERAL INFORMATION:  
APPLICANT: Chua, Nam-Hai  
TITLE OF INVENTION: Expression Motifs That Confer  
TITLE OF INVENTION: Tissue- and Developmental-Specific Expression in Plants  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,986  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/982,792  
FILING DATE: 30-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 3288-019  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: Opaque 2 binding site

US-08-378-986-6

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CTACGTGTA 15  
| | | | | | | |  
Db 2 CTACGTGGA 10

RESULT 99

US-08-388-353-495/c  
; Sequence 495, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 495:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-495

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGT 23  
| | | | | | | |  
Db 10 ACAGGGTGT 2

RESULT 100

US-08-388-353-496/c  
; Sequence 496, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.

; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 496:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-496

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGT 23  
| | | | | | | |  
Db 9 ACAGGGTGT 1

RESULT 101

US-08-388-353-657/c  
; Sequence 657, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995

```
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 657:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-657

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GTACAGGCA 21
DB 10 GTACAGGCA 2

RESULT 102
US-08-388-353-658/c
; Sequence 658, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 661:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-661

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACAGG 20
DB 2 TGTACTGG 10

RESULT 104
US-08-388-353-662
; Sequence 662, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
```

```

; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 662:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-662

```

```

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACAGG 20
DB 1 TGTACTGGG 9

```

```

RESULT 105
US-08-488-551B-495/C
; Sequence 495, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994

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; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 495:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-495

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGT 23
DB 10 ACAGGGTGT 2

```

```

RESULT 106
US-08-488-551B-496/C
; Sequence 496, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 496:

```

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-488-551B-496

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 ACAGGGAGT 23  
| | | | | | | | | |  
Db 9 ACAGGGTGT 1

## RESULT 107

US-08-488-551B-657/c  
; Sequence 657, Application US/08488551B  
; Patent No. 6015661  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Deacon  
; APPLICANT: Dale A. McPhee  
; APPLICANT: David Cooper  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 841  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 GARDEN CITY PLAZA  
; CITY: GARDEN CITY  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 11530-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,551B  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PM3864 (AU)  
; FILING DATE: 14-FEB-1994  
; APPLICATION NUMBER: PM4002 (AU)  
; FILING DATE: 21-FEB-1994  
; APPLICATION NUMBER: PM0284 (AU)  
; FILING DATE: 23-DEC-1994  
; APPLICATION NUMBER: US 08/388,353  
; FILING DATE: 14-FEB-1995  
; APPLICATION NUMBER: PM3021/95  
; FILING DATE: 17-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FRANK S. DIGIGLIO  
; REFERENCE/DOCKET NUMBER: 9606Z  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; INFORMATION FOR SEQ ID NO: 657:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-488-551B-657

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 GTACAGGGA 21

Db 10 GTACAGGCA 2  
| | | | | | | | | |

## RESULT 108

US-08-488-551B-658/c  
; Sequence 658, Application US/08488551B  
; Patent No. 6015661  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Deacon  
; APPLICANT: Dale A. McPhee  
; APPLICANT: David Cooper  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 841  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 GARDEN CITY PLAZA  
; CITY: GARDEN CITY  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 11530-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,551B  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PM3864 (AU)  
; FILING DATE: 14-FEB-1994  
; APPLICATION NUMBER: PM4002 (AU)  
; FILING DATE: 21-FEB-1994  
; APPLICATION NUMBER: PM0284 (AU)  
; FILING DATE: 23-DEC-1994  
; APPLICATION NUMBER: US 08/388,353  
; FILING DATE: 14-FEB-1995  
; APPLICATION NUMBER: PM3021/95  
; FILING DATE: 17-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FRANK S. DIGIGLIO  
; REFERENCE/DOCKET NUMBER: 9606Z  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; INFORMATION FOR SEQ ID NO: 658:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-488-551B-658

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 GTACAGGGA 21  
| | | | | | | | | |

Db 9 GTACAGGCA 1  
| | | | | | | | | |

## RESULT 109

US-08-488-551B-661  
; Sequence 661, Application US/08488551B  
; Patent No. 6015661  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Deacon  
; APPLICANT: Dale A. McPhee  
; APPLICANT: David Cooper  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

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;
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 96062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
;
; INFORMATION FOR SEQ ID NO: 661:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
; US-08-488-551B-661
;
; Query Match 26.4%; Score 7.4; DB 1; Length 10;
; Best Local Similarity 88.9%; Pred. No. 66;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 12 TGTACAGGG 20
; Db 2 TGTACTGGG 10
;
; RESULT 110
; US-08-488-551B-662
; Sequence 662, Application US/08488551B
; Patent No. 6015661
;
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 96062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
;
; INFORMATION FOR SEQ ID NO: 661:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
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; US-08-488-551B-661
;
; Query Match 26.4%; Score 7.4; DB 1; Length 10;
; Best Local Similarity 88.9%; Pred. No. 66;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 12 TGTACAGGG 20
; Db 2 TGTACTGGG 10
;
; RESULT 110
; US-08-488-551B-662
; Sequence 662, Application US/08488551B
; Patent No. 6015661
;
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 96062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
;
; INFORMATION FOR SEQ ID NO: 661:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
; US-08-488-551B-662
;
; Query Match 26.4%; Score 7.4; DB 1; Length 10;
; Best Local Similarity 88.9%; Pred. No. 66;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 12 TGTACAGGG 20
; Db 1 TGTACTGGG 9
;
; RESULT 111
; US-08-488-551B-813/c
; Sequence 813, Application US/08488551B
; Patent No. 6015661
;
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 96062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
;
; INFORMATION FOR SEQ ID NO: 662:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
; US-08-488-551B-662

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 96062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
;
; INFORMATION FOR SEQ ID NO: 662:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
; US-08-488-551B-662
;
; Query Match 26.4%; Score 7.4; DB 1; Length 10;
; Best Local Similarity 88.9%; Pred. No. 66;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 12 TGTACAGGG 20
; Db 1 TGTACTGGG 9
;
; RESULT 111
; US-08-488-551B-813/c
; Sequence 813, Application US/08488551B
; Patent No. 6015661
;
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 96062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
;
; INFORMATION FOR SEQ ID NO: 662:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
; US-08-488-551B-662

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QY 10 CCGTGTACAG 18  
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Db 10 CATGTACAG 2

RESULT 115  
US-09-154-750A-17/c  
; Sequence 17, Application US/09154750A  
; Patent No. 6432640  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Polyak, Kornelia  
; TITLE OF INVENTION: p53-Induced Apoptosis  
; FILE REFERENCE: 1107.75357  
; CURRENT APPLICATION NUMBER: US/09/154,750A  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/059,153  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/079817  
; PRIOR FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-154-750A-17

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGGAGTC 24  
| | | | | | | |  
Db 10 CAGGGAGTC 2

RESULT 116  
US-09-154-750A-37  
; Sequence 37, Application US/09154750A  
; Patent No. 6432640  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Polyak, Kornelia  
; TITLE OF INVENTION: p53-Induced Apoptosis  
; FILE REFERENCE: 1107.75357  
; CURRENT APPLICATION NUMBER: US/09/154,750A  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/059,153  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/079817  
; PRIOR FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-154-750A-37

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGTGTAC 16  
| | | | | | | |  
Db 2 TAAGGTAC 10

RESULT 117  
US-09-462-561B-26/c

; Sequence 26, Application US/09462561B  
; Patent No. 6455252  
; GENERAL INFORMATION:  
; APPLICANT: Wade, Nicholas M.  
; APPLICANT: Harrison, Bruce T.  
; APPLICANT: King, Brian W.  
; APPLICANT: Reed, Kenneth C.  
; APPLICANT: Murphy, Kathleen M.  
; TITLE OF INVENTION: DETERMINATION OF GENETIC SEX IN EQUINE SPECIES BY  
; FILE REFERENCE: ANALYSIS OF Y-CHROMOSOMAL DNA SEQUENCES  
; CURRENT APPLICATION NUMBER: US/09/462,561B  
; CURRENT FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: P07802  
; PRIOR FILING DATE: 1997-07-09  
; PRIOR APPLICATION NUMBER: PCT/AU98/00533  
; PRIOR FILING DATE: 1998-07-08  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Equus caballus  
US-09-462-561B-26

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCTACGTC 13  
| | | | | | | |  
Db 10 CCGTACGTC 2

RESULT 118  
US-09-301-721A-27/c  
; Sequence 27, Application US/09301721A  
; Patent No. 6508561  
; GENERAL INFORMATION:  
; APPLICANT: CHEVAL, Lydie  
; APPLICANT: ELALOUF, Jean-Marc  
; APPLICANT: VIRLON, Berangere  
; TITLE OF INVENTION: MICROASSAY FOR SERIAL ANALYSIS OF GENE EXPRESSION AND  
; FILE REFERENCE: 0846-0499-0X  
; CURRENT APPLICATION NUMBER: US/09/301,721A  
; CURRENT FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: BFO 99400189.9  
; PRIOR FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthetic DNA  
US-09-301-721A-27

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GTACAGGGA 21  
| | | | | | | |  
Db 10 GCACAGGGA 2

RESULT 119  
US-09-508-753B-160/c  
; Sequence 160, Application US/09508753B  
; Patent No. 654736  
; GENERAL INFORMATION:

```
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: YUKO SHIBATA
; APPLICANT: HIROKO FUNAKI
; APPLICANT: EIJI OHARA
; APPLICANT: Masanori WATAHAKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 160
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-160

Query Match      26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 GGATCCAG 27
Db 10 GGAGTTCAG 2

RESULT 120
US-09-769-482-18/c
; Sequence 18, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-769-482-18

Query Match      26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GTGTACAG 19
Db 9 GGGTACAG 1

RESULT 121
US-09-504-132-10/c
; Sequence 10, Application US/09504132
; Patent No. 6582899
; GENERAL INFORMATION:
; APPLICANT: Karb, Carl Alexander
; APPLICANT: Caponigro, Giordano Michael
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS THAT CAUSE A LETHAL
; FILE REFERENCE: 29345/36169
; CURRENT APPLICATION NUMBER: US/09/504,132
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic -
US-09-504-132-10

Query Match      26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 GAGTCCAGG 28
Db 10 GAGTCCAGG 2

RESULT 122
US-09-989-789-1630
; Sequence 1630, Application US/09989789
; Patent No. 6589746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1630

Query Match      26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 17 AGGAGTCC 25
Db 2 AGGAGTTC 10

RESULT 123
US-09-989-789-1631
; Sequence 1631, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1631
; LENGTH: 10
```

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: example target  
OTHER INFORMATION: DNA  
US-09-989-789-1631

Query Match 26.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 AGGAGTCC 25  
|||||  
Db 2 AGGAGTTC 10

RESULT 124  
US-07-951-715A-55/C  
Sequence 55, Application US/07951715A  
Patent No. 5625136  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Wright, Martha S.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/951,715A  
FILING DATE: 25-SEP-1992  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
TELEPHONE: (919)541-8615  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "primer for third quarter -  
first half"  
HYPOTHEtical: NO  
US-07-951-715A-55

Query Match 26.4%; Score 7.4; DB 1; Length 11;  
Best Local Similarity 88.9%; Pred. No. 80;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 TACAGGAG 22  
|||||  
Db 11 TACAGGGG 3

RESULT 125  
US-08-459-448A-55/C  
Sequence 55, Application US/08459448A  
Patent No. 5859336  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5859336artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
STREET: Rd., POB 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,448A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

```

;
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer for third quarter -
; DESCRIPTION: first half"
; HYPOTHETICAL: NO
US-08-459-448A-55

Query Match 26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 TACAGGGGAG 22
Db 11 TACAGGGGG 3

RESULT 126
US-08-459-595A-55/c
; Sequence 55, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6018104artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
```

```

;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer for third quarter -
; DESCRIPTION: first half"
; HYPOTHETICAL: NO
US-08-459-595A-55

Query Match 26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 TACAGGGGAG 22
Db 11 TACAGGGGG 3

RESULT 127
US-08-459-504B-55/c
; Sequence 55, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6075185artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,504B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
```

```
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer for third quarter -
; first half"
; HYPOTHETICAL: NO
; US-08-459-504B-55

Query Match          26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 TACAGGGGAG 22
Db      11 TACAGGGGG 3

RESULT 128
US-08-459-444-55/c
; Sequence 55, Application US/08459444A
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer for third quarter -
; first half"
; HYPOTHETICAL: NO
; US-08-459-504B-55

Query Match          26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 TACAGGGGAG 22
Db      11 TACAGGGGG 3

RESULT 129
US-09-547-422-55/c
; Sequence 55, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer for third quarter -
; first half"
; HYPOTHETICAL: NO
; US-08-459-444-55
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US-09-547-422-55

Query Match 26.4%; Score 7.4; DB 1; Length 11;  
 Best Local Similarity 88.9%; Pred. No. 80;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 TACAGGGAG 22  
 Db 11 TACAGGGG 3

RESULT 130

US-09-153-242-29  
 ; Sequence 29, Application US/09153242  
 ; Patent No. 6482592  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lundberg, Joakim  
 ; TITLE OF INVENTION: MODULAR PROBES II  
 ; FILE REFERENCE: 1181-242  
 ; CURRENT APPLICATION NUMBER: US/09/153,242  
 ; CURRENT FILING DATE: 1998-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/GB97/02629  
 ; PRIOR FILING DATE: 1997-09-26  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 29  
 ; LENGTH: 11  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: oligonucleotide Hi-11  
 US-09-153-242-29

Query Match 26.4%; Score 7.4; DB 1; Length 11;  
 Best Local Similarity 88.9%; Pred. No. 80;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGCCCTAC 10  
 Db 3 GGGCCCTCC 11

RESULT 131

US-09-249-155A-61/c  
 ; Sequence 61, Application US/09249155A  
 ; Patent No. 6538173  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Heber-Katz, Ellen  
 ; TITLE OF INVENTION: Compositions and Methods for Wound  
 ; FILE REFERENCE: 00486.78503  
 ; CURRENT APPLICATION NUMBER: US/09/249,155A  
 ; CURRENT FILING DATE: 1999-02-12  
 ; PRIOR APPLICATION NUMBER: US 60/074,737  
 ; PRIOR FILING DATE: 1998-02-13  
 ; PRIOR APPLICATION NUMBER: US 60/097,937  
 ; PRIOR FILING DATE: 1998-08-26  
 ; PRIOR APPLICATION NUMBER: US 60/102,051  
 ; PRIOR FILING DATE: 1998-09-28  
 ; NUMBER OF SEQ ID NOS: 346  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 61  
 ; LENGTH: 11  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-09-249-155A-61

Query Match 26.4%; Score 7.4; DB 1; Length 11;  
 Best Local Similarity 88.9%; Pred. No. 80;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GTGTACAGG 19  
 Db 11 GTGTCCAGG 3

RESULT 132

US-09-249-155A-162  
 ; Sequence 162, Application US/09249155A  
 ; Patent No. 6538173  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Heber-Katz, Ellen  
 ; TITLE OF INVENTION: Compositions and Methods for Wound  
 ; FILE REFERENCE: 00486.78503  
 ; CURRENT APPLICATION NUMBER: US/09/249,155A  
 ; CURRENT FILING DATE: 1999-02-12  
 ; PRIOR APPLICATION NUMBER: US 60/074,737  
 ; PRIOR FILING DATE: 1998-02-13  
 ; PRIOR APPLICATION NUMBER: US 60/097,937  
 ; PRIOR FILING DATE: 1998-08-26  
 ; PRIOR APPLICATION NUMBER: US 60/102,051  
 ; PRIOR FILING DATE: 1998-09-28  
 ; NUMBER OF SEQ ID NOS: 346  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 162  
 ; LENGTH: 11  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-09-249-155A-162

Query Match 26.4%; Score 7.4; DB 1; Length 11;  
 Best Local Similarity 88.9%; Pred. No. 80;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 GTACAGGGA 21  
 Db 3 GTCCAGGGA 11

RESULT 133

US-09-249-155A-203/c  
 ; Sequence 203, Application US/09249155A  
 ; Patent No. 6538173  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Heber-Katz, Ellen  
 ; TITLE OF INVENTION: Compositions and Methods for Wound  
 ; FILE REFERENCE: 00486.78503  
 ; CURRENT APPLICATION NUMBER: US/09/249,155A  
 ; CURRENT FILING DATE: 1999-02-12  
 ; PRIOR APPLICATION NUMBER: US 60/074,737  
 ; PRIOR FILING DATE: 1998-02-13  
 ; PRIOR APPLICATION NUMBER: US 60/097,937  
 ; PRIOR FILING DATE: 1998-08-26  
 ; PRIOR APPLICATION NUMBER: US 60/102,051  
 ; PRIOR FILING DATE: 1998-09-28  
 ; NUMBER OF SEQ ID NOS: 346  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 203  
 ; LENGTH: 11  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-09-249-155A-203

Query Match 26.4%; Score 7.4; DB 1; Length 11;  
 Best Local Similarity 88.9%; Pred. No. 80;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GTGTACAGG 19  
 Db 11 GTGTCCAGG 3

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA oligonucleotide"
US-08-633-792A-6
Query Match 26.4%; Score 7.4; DB 1; Length 18;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 11 GTGTACAGGGAGTCCAG 27
Db 2 GTGACTCGCTGTACAG 18

RESULT 136
US-09-075-717A-6
; Sequence 6, Application US/09075717A
; Patent No. 6174869
; GENERAL INFORMATION:
; APPLICANT: Barrett, Graham L
; TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE SURVIVAL
; TITLE OF INVENTION: AND AGENTS USEFUL FOR SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,717A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/633,792
; FILING DATE: 01-JUL-1996
; APPLICATION NUMBER: AU PM/1870
; FILING DATE: 18-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516)742-4343
; TELEFAX: (516)742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA oligonucleotide"
US-09-075-717A-6
Query Match 26.4%; Score 7.4; DB 1; Length 18;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 11 GTGTACAGGGAGTCCAG 27
Db 2 GTGACTCGCTGTACAG 18

; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-231
Query Match 26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGGAGTC 24
Db 11 CAGGGAGAC 3

RESULT 135
US-08-633-792A-6
; Sequence 6, Application US/08633792A
; Patent No. 5837694
; GENERAL INFORMATION:
; APPLICANT: Barrett, Graham L
; TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE SURVIVAL
; TITLE OF INVENTION: AND AGENTS USEFUL FOR SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,792A
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PM/1870
; FILING DATE: 18-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516)742-4343
; TELEFAX: (516)742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
```

```

RESULT 137
US-08-327-525A-35
; Sequence 35, Application US/08327525A
; Patent No. 5795716
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark S.
; APPLICANT: Wang, Chunwei
; APPLICANT: Jevons, Luis C.
; APPLICANT: Bernhart, Derek H.
; APPLICANT: Lipshutz, Robert J.
; TITLE OF INVENTION: Computer-Aided Visualization and
; TITLE OF INVENTION: Analysis System for Sequence Evaluation
; Patent No. 5795716
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,525A
; FILING DATE: October 21, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5795716viel, Vernon A.
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528X-82
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-327-525A-35
;
Query Match 25.7%; Score 7.2; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAG 22
Db 1 ACAGGGRR 8

RESULT 138
US-08-531-137B-35
; Sequence 35, Application US/08531137B
; Patent No. 5974164
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark S.
; TITLE OF INVENTION: Computer-Aided Visualization and
; TITLE OF INVENTION: Analysis System for Sequence Evaluation
; Patent No. 5974164
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ritter, Van Pelt & Yi LLP
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; STATE: California
; COUNTRY: USA
; ZIP: 94022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,765
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/531,137
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: AFFYP006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,137B
; FILING DATE: October 16, 1995
; CLASSIFICATION: 382
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: AFFYP006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-531-137B-35
;
Query Match 25.7%; Score 7.2; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAG 22
Db 1 ACAGGGRR 8

RESULT 139
US-09-158-765-35
; Sequence 35, Application US/09158765
; Patent No. 6242180
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark S.
; TITLE OF INVENTION: Computer-Aided Visualization and
; TITLE OF INVENTION: Analysis System for Sequence Evaluation
; Patent No. 6242180
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ritter, Van Pelt & Yi LLP
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; STATE: California
; COUNTRY: USA
; ZIP: 94022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,765
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/531,137
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: AFFYP006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-09-158-765-35

Query Match      25.7%; Score 7.2; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      15 ACAGGGAG 22
Db      1 ACAGGGRR 8

RESULT 140
US-09-796-071-35
; Sequence 35, Application US/09796071
; Patent No. 6607887
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark S.
; TITLE OF INVENTION: Computer-Aided Visualization and
; Analysis System for Sequence Evaluation
; Patent No. 6607887
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ritter, Van Pelt & Yi LLP
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; STATE: California
; COUNTRY: USA
; ZIP: 94022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/796,071
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/531,137
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: APTYP006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-796-071-35

Query Match      25.7%; Score 7.2; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      15 ACAGGGAG 22
Db      1 ACAGGGRR 8

RESULT 141
US-09-281-418-107
; Sequence 107, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA
; TITLE OF INVENTION: agent, Method of Assaying Microorganisms, Method of Analyzing
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER FILING DATE: 1998-03-31
; EARLIER FILING DATE: 1998-03-31
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 107
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-107

Query Match      25.7%; Score 7.2; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      11 GTGTACAGGGAG 22
Db      1 GAGTACAGGAG 12

RESULT 142
US-09-281-418-25
; Sequence 25, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA
; TITLE OF INVENTION: agent, Method of Assaying Microorganisms, Method of Analyzing
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER FILING DATE: 1998-03-31
; EARLIER FILING DATE: 1998-03-31
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 25
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-25

Query Match      25.7%; Score 7.2; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      12 TGTACAGGGAGT 23
Db      1 TCTACAGGAGT 12

RESULT 143
US-08-182-968A-297/c
; Sequence 297, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION

```

NUMBER OF SEQUENCES: 497  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,968A  
FILING DATE: 13-JANUARY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,888  
FILING DATE: 14-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 205/277  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 297:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-182-968A-297

Query Match 25.7%; Score 7.2; DB 1; Length 15;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCA 26  
Db 13 ACCTGGACTCCA 2

RESULT 144  
US-08-774-306A-297/c  
Sequence 297, Application US/08774306A  
Patent No. 5869253  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 497  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 07/882,888  
FILING DATE: April 21, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/774,306  
FILING DATE: December 26, 1996  
APPLICATION NUMBER: 08/182,968  
FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882,888  
FILING DATE: May 14, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 234/083  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 297:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/182,968  
FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882,888  
FILING DATE: May 14, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 223/227  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 297:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-774-306A-297

Query Match 25.7%; Score 7.2; DB 1; Length 15;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCA 26  
Db 13 ACCTGGACTCCA 2

RESULT 145  
US-09-064-156A-297/c  
Sequence 297, Application US/09064156A  
Patent No. 6132966  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 498  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/064,156A  
FILING DATE: April 21, 1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/774,306  
FILING DATE: December 26, 1996  
APPLICATION NUMBER: 08/182,968  
FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882,888  
FILING DATE: May 14, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 234/083  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 297:

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-064-156A-297

Query Match 25.7%; Score 7.2; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 15 ACAGGAGTCCA 26
Db 13 ACCTGGACTCCA 2

RESULT 146
US-08-859-954-179
; Sequence 179, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 179:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-179

Query Match 25.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 AGTCCAG 27
Db 7 AGTCCAG 1

RESULT 148
US-08-859-954-436
; Sequence 436, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
```

```

; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 436:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-859-954-436

Query Match 25.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e-02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AGTCCAG 27
Db 1 AGTCCAG 7

RESULT 149
US-08-859-954-437
; Sequence 437, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 436:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-859-954-436
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 437:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-859-954-437

Query Match 25.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e-02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AGTCCAG 27
Db 1 AGTCCAG 7

RESULT 150
US-08-859-954-510/c
; Sequence 510, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 510:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-859-954-437
```

```

; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-859-954-510

Query Match 25.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AGGGAGT 23
DB 7 AGGGAGT 1

RESULT 151
US-09-878-693-5/c
; Sequence 5, Application US/09878693
; Patent No. 6677510
; GENERAL INFORMATION:
; APPLICANT: Windham, Mark T.
; APPLICANT: Trigiano, Robert N.
; APPLICANT: Witte, Willard T.
; TITLE OF INVENTION: Powdery Mildew Resistant Plants
; FILE REFERENCE: UTR-101X
; CURRENT APPLICATION NUMBER: US/09/878,693
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 60/210,603
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Random Primer
; US-09-878-693-5

Query Match 25.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCTAGCT 12
DB 8 CCTAGCT 2

RESULT 152
US-08-331-398A-37/c
; Sequence 37, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION NUMBER: US 07/767,331
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-1261100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-331-398A-37

Query Match 25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGGAG 22
DB 9 CAGGGAG 3

RESULT 153
US-08-605-163-11/c
; Sequence 11, Application US/08605163
; Patent No. 5879886
; GENERAL INFORMATION:
; APPLICANT: Meo, Tommaso
; APPLICANT: Tosi, Mario
; APPLICANT: Verpy, Elisabeth
; APPLICANT: Biasotto, Michel
; TITLE OF INVENTION: Method for Detecting Molecules
; TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of These
; TITLE OF INVENTION: Mismatches, and Application to the Detection of Base
; TITLE OF INVENTION: Substitutions or Deletions in Nucleotide Sequences.
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,163
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05986.0005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs

```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-605-163-11
Query Match      25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 ACAGGGA 21
DB      8 ACAGGGA 2

RESULT 154
US-08-605-163-12/c
; Sequence 12, Application US/08605163
; Patent No. 5879886
; GENERAL INFORMATION:
; APPLICANT: Meo, Tommaso
; APPLICANT: Tosi, Mario
; APPLICANT: Verpy, Elisabeth
; APPLICANT: Biasotto, Michel
; TITLE OF INVENTION: Method for Detecting Molecules
; TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of These
; TITLE OF INVENTION: Mismatches, and Application to the Detection of Base
; TITLE OF INVENTION: Substitutions or Deletions in Nucleotide Sequences.
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,163
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05986.0005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-605-163-12

Query Match      25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 ACAGGGA 21
DB      8 ACAGGGA 2

RESULT 155
US-08-331-397B-37/c
```

```
; Sequence 37, Application US/08331397B
; Patent No. 5984726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,438
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-331-397B-37

Query Match      25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 CAGGGAG 22
DB      9 CAGGGAG 3

RESULT 156
US-08-759-804A-37/c
; Sequence 37, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```

```
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-759-804A-37

Query Match 25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGGAG 22
DB 9 CAGGGAG 3

RESULT 157
US-09-046-858A-3
; Sequence 3, Application US/09046858A
; Patent No. 6048973
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; TITLE OF INVENTION: IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/042,376
```

```
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0860
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-046-858A-3

Query Match 25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTACGTG 13
DB 1 CTACGTG 7

RESULT 158
US-09-227-693-37/C
; Sequence 37, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,693
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,396
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
```

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-09-227-693-37

Query Match 25.0%; Score 7; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGGAG 22  
| | | | |  
DB 9 CAGGGAG 3

## RESULT 159

US-09-153-242-33  
; Sequence 33, Application US/09153242  
; Patent No. 6482592

; GENERAL INFORMATION:  
; APPLICANT: Lundberg, Joakim  
; APPLICANT: Uhlen, Mathias  
; TITLE OF INVENTION: MODULAR PROBES II  
; FILE REFERENCE: 1181-242  
; CURRENT APPLICATION NUMBER: US/09/153,242  
; CURRENT FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: PCT/GB97/02629  
; FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide H3  
US-09-153-242-33

Query Match 25.0%; Score 7; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCT 8  
| | | | |  
DB 2 GGGCCCT 8

## RESULT 160

US-09-989-789-2121  
; Sequence 2121, Application US/09989789  
; Patent No. 6588746

; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2121  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-2121

Query Match 25.0%; Score 7; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGGAG 22  
| | | | |  
DB 1 CAGGGAG 7

## RESULT 161

US-09-989-789-2122  
; Sequence 2122, Application US/09989789  
; Patent No. 6588746

; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2122  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-2122

Query Match 25.0%; Score 7; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGGAG 22  
| | | | |  
DB 1 CAGGGAG 7

## RESULT 162

US-09-989-789-2330  
; Sequence 2330, Application US/09989789  
; Patent No. 6588746

; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2330  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-2330

Query Match 25.0%; Score 7; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25  
| | | | |  
DB 3 GGAGTCC 9

## RESULT 163

US-09-989-789-2331  
; Sequence 2331, Application US/09989789  
; Patent No. 6588746

; GENERAL INFORMATION:



APPLICANT: LIU, Qiang  
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
FILE REFERENCE: 8325-0011.20 / S11-US2  
CURRENT FILING DATE: 2002-03-25  
NUMBER OF SEQ ID NOS: 4085  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2331  
LENGTH: 9  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: example target  
US-09-989-789-2331

Query Match 25.0%; Score 7; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25  
| | | | |  
Db 3 GGAGTCC 9

RESULT 164  
US-09-989-789-2347  
Sequence 2347, Application US/09989789  
Patent No. 6588746  
GENERAL INFORMATION:

APPLICANT: LIU, Qiang  
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
FILE REFERENCE: 8325-0011.20 / S11-US2  
CURRENT FILING DATE: 2002-03-25  
NUMBER OF SEQ ID NOS: 4085  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2347  
LENGTH: 9  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: example target  
US-09-989-789-2347

Query Match 25.0%; Score 7; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25  
| | | | |  
Db 3 GGAGTCC 9

RESULT 165  
US-09-989-789-2348  
Sequence 2348, Application US/09989789  
Patent No. 6588746  
GENERAL INFORMATION:  
APPLICANT: LIU, Qiang  
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
FILE REFERENCE: 8325-0011.20 / S11-US2  
CURRENT FILING DATE: 2002-03-25  
NUMBER OF SEQ ID NOS: 4085  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2348  
LENGTH: 9  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: example target  
US-09-989-789-2348

Query Match 25.0%; Score 7; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25  
| | | | |  
Db 3 GGAGTCC 9

RESULT 166  
US-09-450-515-3  
Sequence 3, Application US/09450515  
Patent No. 6680425  
GENERAL INFORMATION:  
APPLICANT: Rodriguez, Raymond L.  
TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES  
IN ALPHA-AMYLASE GENES

NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: PO Box 60850  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/450,515  
FILING DATE: 29-No. 6680425-1999  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/046,858  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J.  
REGISTRATION NUMBER: 28,006  
REFERENCE/DOCKET NUMBER: 2000-0456.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-450-515-3

Query Match 25.0%; Score 7; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTAGGTG 13  
| | | | |  
Db 1 CTAGGTG 7

RESULT 167  
US-09-263-790-19/c  
Sequence 19, Application US/09263790  
Patent No. PPI2997

```

; GENERAL INFORMATION:
; APPLICANT: Nirmal Kumar PATRA et al.
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
; FILE REFERENCE: 2761-0120P
; CURRENT APPLICATION NUMBER: US/09/263,790
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MAP 19 Primer - Primer used in RAPD analysis comparing Jal Pallav
; OTHER INFORMATION: with Jorlab-2, Manjusha, Mandakini, Bio-13, and Ceylon.
US-09-263-790-19

```

```

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 19 GGAGTCC 25
    |||||
Db 7 GGAGTCC 1

```

## RESULT 168

```

US-09-538-341-12/c
; Sequence 12, Application US/09538341
; Patent No. PP13110
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sushil
; APPLICANT: Bahl, Janak Paj
; APPLICANT: Bansal, Ravi Prakash
; APPLICANT: Niwas, Shri
; APPLICANT: Naqvi, Arif Ali
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Singh, Vikram
; APPLICANT: Sinha, Shweta
; TITLE OF INVENTION: Lippia alba plant named 'Bhurakshak'
; FILE REFERENCE: U-012701-4
; CURRENT APPLICATION NUMBER: US/09/538,341
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for generating random amplified polymorphic DNA profile of
; OTHER INFORMATION: plant
US-09-538-341-12

```

```

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 19 GGAGTCC 25
    |||||
Db 7 GGAGTCC 1

```

## RESULT 169

```

US-09-785-716A-18/c
; Sequence 18, Application US/09785716A
; Patent No. PP14090
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; APPLICANT: Dwivedi, Samresh
; APPLICANT: Singh, Maneesha
; APPLICANT: Singh, Ajay Pratap

```

```

; APPLICANT: Singh, Vandana
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Naqvi, Ali Arif
; APPLICANT: Kuman, Sushil
; TITLE OF INVENTION: New Peppermint Plant Named 'PRANJAL'
; FILE REFERENCE: 41799/VGG/K375
; CURRENT APPLICATION NUMBER: US/09/785,716A
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for RAPD profile
US-09-785-716A-18

```

```

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 19 GGAGTCC 25
    |||||
Db 7 GGAGTCC 1

```

## RESULT 170

```

US-09-799-880-19/c
; Sequence 19, Application US/09799880
; Patent No. PP14400
; GENERAL INFORMATION:
; APPLICANT: Gupta, Ritika
; APPLICANT: Sastri, Kakaraparthi
; APPLICANT: Banerjee, Suchitra
; APPLICANT: Mallavarapu, Gopal
; APPLICANT: Ramesh, Srinivas
; APPLICANT: Shasany, Ajit
; APPLICANT: Darokar, Mahendra
; APPLICANT: Khanuja, Suman
; TITLE OF INVENTION: A NOVEL ROSE SCENTED GERANIUM PELARGONIUM GRAVEOLENS PLANT 'SAF'
; FILE REFERENCE: 2734-102
; CURRENT APPLICATION NUMBER: US/09/799,880
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-799-880-19

```

```

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 19 GGAGTCC 25
    |||||
Db 7 GGAGTCC 1

```

## RESULT 171

```

US-08-590-571-19/c
; Sequence 19, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:

```

ADDRESS: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,571  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: Yale  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-590-571-19

Query Match 25.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGAGTC 24  
Db 9 GGGAGTC 3

RESULT 172  
US-08-590-571-31/c  
Sequence 31, Application US/08590571  
Patent No. 5861246  
GENERAL INFORMATION:  
APPLICANT: Sherman Weissman and Girish N. Nallur  
TITLE OF INVENTION: MULTIPLE SELECTION PROCESS  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,571  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: Yale  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-590-571-31

Query Match 25.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGAGTC 24  
Db 9 GGGAGTC 3

RESULT 173  
US-08-388-353-659/c  
Sequence 659, Application US/08388353  
Patent No. 6010895  
GENERAL INFORMATION:  
APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DiGiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 659:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-659

Query Match 25.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GTACAGG 19  
Db 8 GTACAGG 2

RESULT 174  
US-08-388-353-660/c  
Sequence 660, Application US/08388353

```

; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Leamont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 660:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-660

Query Match 25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GTACAGG 19
Db 7 GTACAGG 1

RESULT 175
US-08-468-856B-14
; Sequence 14, Application US/08468856B
; Patent No. 6013772
; GENERAL INFORMATION:
; APPLICANT: Barnett, Thomas; Elting, James; Kamarch, Michael;
; APPLICANT: Kretschmer, Axel
; TITLE OF INVENTION: CDNAS CODING FOR MEMBERS OF THE
; TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spring Horn Kramer & Woods
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 Mb storage
; COMPUTER: APPLE MACINTOSH 6500
; OPERATING SYSTEM: SYSTEM 7.5
; SOFTWARE: WordPerfect 3.5

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,856B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,974
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/760,031
; FILING DATE: 13-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/274,107
; FILING DATE: 21-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/207,678
; FILING DATE: 16-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/060,031
; FILING DATE: 19-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/016,683
; FILING DATE: 19-FEB-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/896,361
; FILING DATE: 13-AUG-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: MDI 242.10-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-468-856B-14

Query Match 25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCT 8
Db 1 GGGCCCT 7

RESULT 176
US-08-488-551B-659/c
; Sequence 659, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B

```

;/ FILING DATE: 07-JUN-1995  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: PM3864 (AU)  
;/ FILING DATE: 14-FEB-1994  
;/ APPLICATION NUMBER: PM4002 (AU)  
;/ FILING DATE: 21-FEB-1994  
;/ APPLICATION NUMBER: PM0284 (AU)  
;/ FILING DATE: 23-DEC-1994  
;/ APPLICATION NUMBER: US 08/388,353  
;/ FILING DATE: 14-FEB-1995  
;/ APPLICATION NUMBER: PM3021/95  
;/ FILING DATE: 17-MAY-1995  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: FRANK S. DIGIGLIO  
;/ REFERENCE/DOCKET NUMBER: 9606Z  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (516) 742-4343  
;/ TELEFAX: (516) 742-4366  
;/ INFORMATION FOR SEQ ID NO: 659:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 10 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: DNA  
;/ US-08-488-551B-659

Query Match 25.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GTACAGG 19  
|||  
Db 8 GTACAGG 2

RESULT 177  
US-08-488-551B-660/c  
; Sequence 660, Application US/08488551B  
; Patent No. 6015661  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Deacon  
; APPLICANT: Dale A. McPhee  
; APPLICANT: David Cooper  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 841  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 GARDEN CITY PLAZA  
; CITY: GARDEN CITY  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 11530-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,551B  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PM3864 (AU)  
; FILING DATE: 14-FEB-1994  
; APPLICATION NUMBER: PM4002 (AU)  
; FILING DATE: 21-FEB-1994  
; APPLICATION NUMBER: PM0284 (AU)  
; FILING DATE: 23-DEC-1994  
; APPLICATION NUMBER: US 08/388,353  
; FILING DATE: 14-FEB-1995  
; APPLICATION NUMBER: PM3021/95  
; FILING DATE: 17-MAY-1995  
; ATTORNEY/AGENT INFORMATION:

;/ NAME: FRANK S. DIGIGLIO  
;/ REFERENCE/DOCKET NUMBER: 9606Z  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (516) 742-4343  
;/ TELEFAX: (516) 742-4366  
;/ INFORMATION FOR SEQ ID NO: 660:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 10 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: DNA  
;/ US-08-488-551B-660

Query Match 25.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GTACAGG 19  
|||  
Db 7 GTACAGG 1

RESULT 178  
US-08-468-859A-14  
; Sequence 14, Application US/08468859A  
; Patent No. 602358  
; GENERAL INFORMATION:  
; APPLICANT: Barnett, Thomas; Elting, James; Kamarck, Michael;  
; APPLICANT: Kretschmer, Axel  
; TITLE OF INVENTION: CDNAS CODING FOR MEMBERS OF THE  
; TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sprung Horn Kramer & Woods  
; STREET: 660 White Plains Road  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591-5144  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 Mb storage  
; COMPUTER: APPLE MACINTOSH 6500  
; OPERATING SYSTEM: SYSTEM 7.5  
; SOFTWARE: WordPerfect 3.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,859A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/027,974  
; FILING DATE: 08-MAR-1993  
; APPLICATION NUMBER: US 07/760,031  
; FILING DATE: 13-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/274,107  
; FILING DATE: 21-NOV-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/207,678  
; FILING DATE: 16-JUN-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/060,031  
; FILING DATE: 19-JUN-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/016,683  
; FILING DATE: 19-FEB-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 06/896,361  
; FILING DATE: 13-AUG-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurt G. Briscoe  
; REGISTRATION NUMBER: 33,141

REFERENCE/DOCKET NUMBER: MDI 242.9-KGB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 332-1700  
TELEFAX: (914) 332-1844  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-468-859A-14

Query Match 25.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCT 8  
DB 1 GGGCCCT 7

RESULT 179  
US-08-906-691-10/c  
Sequence 10, Application US/08906691  
Patent No. 6066452  
GENERAL INFORMATION:  
APPLICANT: Weisman, Sherman M.  
APPLICANT: Nallur, Girish N.  
APPLICANT: Kulkarni, Prakash  
TITLE OF INVENTION: MULTIPLEX SELECTION TECHNIQUE FOR  
IDENTIFYING PROTEIN-BINDING SITES FOR DNA-BINDING PROTEINS  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 981094  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/906,691  
FILING DATE: 31-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6066452tenburg Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 390036.403C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-906-691-10

Query Match 25.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGAGTC 24  
DB 9 GGGAGTC 3

RESULT 180  
US-08-522-384-27/c  
Sequence 27, Application US/08522384  
Patent No. 6110667  
GENERAL INFORMATION:  
APPLICANT: LOPEZ-NIETO, CARLOS E  
APPLICANT: NIGAM, SANJAY KUMAR  
TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR  
CHARACTERIZING NUCLEOTIDE SEQUENCES  
TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES  
FILE REFERENCE: 2458-4029  
CURRENT APPLICATION NUMBER: US/08/522,384  
CURRENT FILING DATE: 1996-11-15  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 27  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Unknown Organism  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Primer  
US-08-522-384-27

Query Match 25.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GTCCAGG 28  
DB 7 GTCCAGG 1

RESULT 181  
US-09-154-750A-49  
Sequence 49, Application US/09154750A  
Patent No. 6432640  
GENERAL INFORMATION:  
APPLICANT: Vogelstein, Bert  
APPLICANT: Kinzler, Kenneth  
APPLICANT: Polyak, Kornelia  
TITLE OF INVENTION: p53-Induced Apoptosis  
FILE REFERENCE: 1107.75357  
CURRENT APPLICATION NUMBER: US/09/154,750A  
CURRENT FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/059,153  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/079817  
PRIOR FILING DATE: 1998-03-30  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 49  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-154-750A-49

Query Match 25.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AGGAGT 23  
DB 2 AGGAGT 8

RESULT 182  
US-09-313-221A-136/c  
Sequence 136, Application US/09313221A  
Patent No. 6468743  
GENERAL INFORMATION:  
APPLICANT: Thomas L. Romick (Inventor)  
APPLICANT: Mark S. Fraser (Inventor)  
TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL  
AND VIRAL CONTAMINANTS IN FOODSTUFFS



```
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-538-456-9

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25
    |||||
Db 7 GGAGTCC 1

RESULT 187
US-09-769-482-43
; Sequence 43, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-43

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGAG 22
    |||||
Db 3 CAGGAG 9

RESULT 188
US-09-989-789-1285
; Sequence 1285, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1285
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1314

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCT 8
    |||||
Db 2 GGGCCCT 8

RESULT 189
US-09-989-789-1307
; Sequence 1307, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1307
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1307

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCT 8
    |||||
Db 2 GGGCCCT 8

RESULT 190
US-09-989-789-1314
; Sequence 1314, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1314
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1314

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCT 8
    |||||
Db 2 GGGCCCT 8
```



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; Patent No. PP14090
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; APPLICANT: Dwivedi, Samresh
; APPLICANT: Singh, Maneesha
; APPLICANT: Singh, Ajay Pratap
; APPLICANT: Singh, Vandana
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Naqvi, Ali Arif
; APPLICANT: Kuman, Sushil
; TITLE OF INVENTION: New Peppermint Plant Named 'PRANJAL'
; FILE REFERENCE: 41799/VGG/K375
; CURRENT APPLICATION NUMBER: US/09/785,716A
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for RAPD profile
US-09-785-716A-18

Query Match      24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
DB 1 GGACTCCAGC 10

RESULT 194
US-09-799-980-19
; Sequence 19, Application US/09799880
; Patent No. PP14400
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sushil
; APPLICANT: Gupta, Ritika
; APPLICANT: Sastri, Kakraparthi
; APPLICANT: Banerjee, Suchitra
; APPLICANT: Mallavarapu, Gopal
; APPLICANT: Ramesh, Srinivas
; APPLICANT: Shasany, Ajit
; APPLICANT: Darokar, Mahendra
; APPLICANT: Khanuja, Suman
; TITLE OF INVENTION: A NOVEL ROSE SCENTED GERANIUM PELARGONIUM GRAVEOLENS PLANT 'SAF'
; FILE REFERENCE: 2734-102
; CURRENT APPLICATION NUMBER: US/09/799,880
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-799-880-19

Query Match      24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
DB 1 GGACTCCAGC 10

RESULT 195
US-08-388-353-660
; Sequence 660, Application US/08388353

```

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; Patent No. PP12997
; GENERAL INFORMATION:
; APPLICANT: Nital Kumar PATRA et al.
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
; FILE REFERENCE: 2761-0120P
; CURRENT APPLICATION NUMBER: US/09/263,790
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Map 19 Primer - Primer used in RAPD analysis comparing Jal Pallavi
; OTHER INFORMATION: with Jorlab-2, Manjusha, Mandakini, Bio-13, and Ceylon.
US-09-263-790-19

Query Match      24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
DB 1 GGACTCCAGC 10

RESULT 192
US-09-538-341-12
; Sequence 12, Application US/09538341
; Patent No. PP13110
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sushil
; APPLICANT: Bahl, Janak Faj
; APPLICANT: Bansal, Ravi Prakash
; APPLICANT: Niwas, Shri
; APPLICANT: Naqvi, Arif Ali
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Singh, Vikram
; APPLICANT: Sinha, Shweta
; TITLE OF INVENTION: Lippia alba plant named 'Bhurakshak'
; FILE REFERENCE: U-012701-4
; CURRENT APPLICATION NUMBER: US/09/538,341
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for generating random amplified polymorphic DNA profile of
; OTHER INFORMATION: plant
US-09-538-341-12

Query Match      24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
DB 1 GGACTCCAGC 10

RESULT 193
US-09-785-716A-18
; Sequence 18, Application US/09785716A

```

```
/ Patent No. 6010895
/ GENERAL INFORMATION:
/ APPLICANT: Deacon, Nicholas J.
/ APPLICANT: Leamont, Jennifer C.
/ APPLICANT: McPhee, Dale A.
/ APPLICANT: Crowe, Suzanne
/ APPLICANT: Cooper, David
/ TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
/ NUMBER OF SEQUENCES: 800
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Scully, Scott, Murphy & Presser
/ STREET: 400 Garden City Plaza
/ CITY: Garden City
/ STATE: New York
/ COUNTRY: United States
/ ZIP: 11530
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/388,353
/ FILING DATE: 14-FEB-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Digiglio, Frank S.
/ REGISTRATION NUMBER: 31,346
/ REFERENCE/DOCKET NUMBER: 9606
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 742-4343
/ TELEFAX: (516) 742-4366
/ TELEX: 230 901 SANS UR
/ INFORMATION FOR SEQ ID NO: 660:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-388-353-660

Query Match 24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGGTGACAGG 19
Db 1 CCTGTACTGG 10

RESULT 196
US-08-488-551B-660
/ Sequence 660, Application US/08488551B
/ Patent No. 6015661
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas J. Deacon
/ APPLICANT: Dale A. McPhee
/ APPLICANT: David Cooper
/ TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
/ NUMBER OF SEQUENCES: 841
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
/ STREET: 400 GARDEN CITY PLAZA
/ CITY: GARDEN CITY
/ STATE: NEW YORK
/ COUNTRY: U.S.A.
/ ZIP: 11530-0299
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25

Query Match 24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGGTGACAGG 19
Db 1 CCTGTACTGG 10

RESULT 197
US-09-537-186-13
/ Sequence 13, Application US/09537186
/ Patent No. 6534596
/ GENERAL INFORMATION:
/ APPLICANT: COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
/ TITLE OF INVENTION: A disease resistant high yielding variety Papaver somniferum cal
/ FILE OF INVENTION: Rakshit
/ FILE REFERENCE: Q58615
/ CURRENT APPLICATION NUMBER: US/09/537,186
/ CURRENT FILING DATE: 2000-03-29
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 13
/ LENGTH: 10
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: : Primer for generating ran
/ OTHER INFORMATION: m amplified polymorphic DNA profile of claimed plant
/ US-09-537-186-13

Query Match 24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
Db 1 GGACTCCAGG 10

RESULT 198
US-09-538-456-9
/ Sequence 9, Application US/09538456
/ Patent No. 6558940
```

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; GENERAL INFORMATION:
; APPLICANT: Alam, Mansoor
; APPLICANT: Sattar, Abdul
; APPLICANT: Kumar, Sushil
; APPLICANT: Samad, Abdul
; APPLICANT: Dhanwan, Om Prakash
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Singh, Seema
; APPLICANT: Kumar, Poovappallivadakethil Viswanathan Nair Ajay
; APPLICANT: Khalique, Abdul
; APPLICANT: Zaim, Mohammad
; APPLICANT: Shahabuddin, Saba
; APPLICANT: Trivedi, Mala
; TITLE OF INVENTION: A novel Streptomyces strain with potential anti-microbial
; TITLE OF INVENTION: activity against phytopathogenic fungi
; FILE REFERENCE: 148920.00003
; CURRENT APPLICATION NUMBER: US/09/538/456
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Word-97
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
; US-09-538-456-9

Query Match 24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
Db 1 GGACTCCAGC 10

; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,177
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnet, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-474-177-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTAGGTGACAGG 19
Db 13 CTTCTGGACAGC 1

; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1E1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,033
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086

```

## RESULT 200

US-08-487-033-23/c

; Sequence 23, Application US/08487033

; Patent No. 5739027

; GENERAL INFORMATION:

; APPLICANT: Kamb, Alexander

; TITLE OF INVENTION: MTS1E1-Beta GENE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Venable, Baetjer, Howard &amp; Civiletti, LLP

; STREET: 1201 New York Avenue, Suite 1000

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,033

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/03316

; FILING DATE: 17-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/251,938

; FILING DATE: 01-JUN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/215,087

; FILING DATE: 18-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/215,086

/ FILING DATE: 18-MAR-1994  
/ PRIOR APPLICATION NUMBER: US 08/227,369  
/ FILING DATE: 14-APR-1994  
/ PRIOR APPLICATION DATA:  
/ FILING DATE: 18-MAR-1994  
/ APPLICATION NUMBER: US 08/214,582  
/ FILING DATE: 18-MAR-1994  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Ihnen, Jeffrey L.  
/ REGISTRATION NUMBER: 28,957  
/ REFERENCE/DOCKET NUMBER: 24884-109348-C  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-962-4810  
/ TELEFAX: 202-962-8300  
/ INFORMATION FOR SEQ ID NO: 23:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 16 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (genomic)  
/ HYPOTHETICAL: NO  
/ ANTI-SENSE: YES  
/ ORIGINAL SOURCE:  
/ ORGANISM: Homo sapiens  
/ US-08-487-033-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19  
Db 13 CTTCCTGGACAG 1

RESULT 201  
US-08-810-23/c  
/ Sequence 23, Application US/08480810  
/ Patent No. 5801236  
/ GENERAL INFORMATION:  
/ APPLICANT: Kamb, Alexander  
/ TITLE OF INVENTION: MTS1 GENE  
/ NUMBER OF SEQUENCES: 36  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
/ STREET: 1201 New York Avenue, Suite 1000  
/ CITY: Washington  
/ STATE: DC  
/ COUNTRY: USA  
/ ZIP: 20005  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/480,810  
/ FILING DATE: 07-JUN-1995  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: PCT/US95/03316  
/ FILING DATE: 17-MAR-1995  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/251,938  
/ FILING DATE: 01-JUN-1994  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/215,087  
/ FILING DATE: 18-MAR-1994  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/215,086  
/ FILING DATE: 18-MAR-1994  
/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/227,369  
/ FILING DATE: 14-APR-1994  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/214,582  
/ FILING DATE: 18-MAR-1994  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Ihnen, Jeffrey L.  
/ REGISTRATION NUMBER: 28,957  
/ REFERENCE/DOCKET NUMBER: 24884-109348  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-962-4810  
/ TELEFAX: 202-962-8300  
/ INFORMATION FOR SEQ ID NO: 23:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 16 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (genomic)  
/ HYPOTHETICAL: NO  
/ ANTI-SENSE: YES  
/ ORIGINAL SOURCE:  
/ ORGANISM: Homo sapiens  
/ US-08-480-810-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19  
Db 13 CTTCCTGGACAG 1

RESULT 202  
US-08-508-735-23/c  
/ Sequence 23, Application US/08508735  
/ Patent No. 5843756  
/ GENERAL INFORMATION:  
/ APPLICANT: Stone, Steven  
/ APPLICANT: Jiang, Ping  
/ APPLICANT: Kamb, Alexander  
/ TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF  
/ NUMBER OF SEQUENCES: 47  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
/ STREET: 1201 New York Avenue, Suite 1000  
/ CITY: Washington  
/ STATE: DC  
/ COUNTRY: USA  
/ ZIP: 20005  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/508,735  
/ FILING DATE:  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US to be assigned  
/ FILING DATE: 07-JUN-1995  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: PCT/US95/03316  
/ FILING DATE: 17-MAR-1995  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Ihnen, Jeffrey L.  
/ REGISTRATION NUMBER: 28,957  
/ REFERENCE/DOCKET NUMBER: 24884-109348  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-962-4848  
/ TELEFAX: 202-962-8300

```

/ INFORMATION FOR SEQ ID NO: 23:
/
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: YES
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ US-08-508-735-23

```

Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels

## RESULT 203

US-08-848-251-23/c  
; Sequence 23, Application US/08848251  
; Patent No. 5989815

```

/ / GENERAL INFORMATION:
/ / APPLICANT: Skolnick, Mark H.
/ / APPLICANT: Cannon-Albright, Lisa A.
/ / APPLICANT: Kamb, Alexander
/ / TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
/ / TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO
/ / TITLE OF INVENTION: GENE
/ / NUMBER OF SEQUENCES: 36
/ / CORRESPONDENCE ADDRESS:
/ / ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
/ / STREET: 1201 New York Avenue, Suite 1000
/ / CITY: Washington
/ / STATE: DC
/ / COUNTRY: USA
/ / ZIP: 20005

```

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER ITEM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/848,251  
FILING DATE:

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/ / REFERENCE/DOCKET NUMBER: 24884-109348-G
/ /
/ / TELECOMMUNICATION INFORMATION:
/ /
/ / TELEPHONE: 202-562-4810
/ /
/ / TELEFAX: 202-962-8300
/ /
/ / INFORMATION FOR SEQ ID NO: 23:
/ /
/ / SEQUENCE CHARACTERISTICS:
/ /
/ / LENGTH: 16 base pairs
/ /
/ / TYPE: nucleic acid
/ /
/ / STRANDEDNESS: single
/ /
/ / TOPOLOGY: linear
/ /
/ / MOLECULE TYPE: DNA (genomic)
/ /
/ / HYPOTHETICAL: NO
/ /
/ / ANTI-SENSE: YES
/ /
/ / ORIGINAL SOURCE:
/ /
/ / ORGANISM: Homo sapiens
/ /
/ / US-08-848-251-23

```

Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9: Conservative 0; Mismatches 4; Indels

RESULT 204

US-08-486-047-23/c  
; Sequence 23, Application US/08486047  
; Patent No. 5994095

```

/ GENERAL INFORMATION:
/ APPLICANT: Kamb, Alexander
/ TITLE OF INVENTION: MS2 GENE
/ NUMBER OF SEQUENCES: 36
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Venable, Baetjer, Howard & Civiletti, LLP
/ STREET: 1201 New York Avenue, Suite 1000
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005

```

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/486.047  
APPLICATION NUMBER: US/08/486.047  
FILING DATE: 07-JUN-1995

TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
MOLECULE TYPE: DNA (genomic)  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-486-047-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19  
DB 13 CTTCTGGACAGC 1

## RESULT 205

US-09-120-130-23/c  
Sequence 23, Application US/09120130

Patent No. 6037462

GENERAL INFORMATION:

APPLICANT: Kamb, Alexander

TITLE OF INVENTION: MTS1 GENE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/120,130

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/480,810

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,938

FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,087

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,086

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,369

FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
MOLECULE TYPE: DNA (genomic)  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-120-130-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19  
DB 13 CTTCTGGACAGC 1

## RESULT 206

US-09-115-252-23/c

Sequence 23, Application US/09115252

Patent No. 6080301

GENERAL INFORMATION:

APPLICANT: Kamb, Alexander

TITLE OF INVENTION: MTS1 GENE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/115,252

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/480,810

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: PCT/US95/03316

FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,938

FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,087

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,086

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,369

FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-115-252-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19  
DB 13 CTTCTGGACAG 1

## RESULT 207

US-08-986-515-23/c  
Sequence 23, Application US/08986515  
Patent No. 6090578

GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/986.515  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/480,810  
FILING DATE:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Innen, Jeffrey L.  
REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-986-515-23

Query Match 23.8%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19  
DB 13 CTTCTGGACAG 1

## RESULT 208

US-09-120-128-23/c  
Sequence 23, Application US/09120128  
Patent No. 6140473

GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS2 GENE

NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/120,128  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,047  
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Innen, Jeffrey L.  
REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-120-128-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 CTACGTGTACAGG 19  
Db 13 CTTCTGGACAGC 1

## RESULT 209

US-09-120-129-23/c  
; Sequence 23, Application US/09120129  
; Patent No. 6180776  
; GENERAL INFORMATION:  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: MTS2 GENE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/120,129  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/486,047  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: PCT/US95/03316  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/251,938  
; FILING DATE: 01-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,087  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,086  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,369  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/214,582  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-109348-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-120-129-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 CTACGTGTACAGG 19  
Db 13 CTTCTGGACAGC 1

## RESULT 210

US-09-201-139-23/c  
; Sequence 23, Application US/09201139  
; Patent No. 6210949  
; GENERAL INFORMATION:  
; APPLICANT: Stone, Steven  
; APPLICANT: Jiang, Ping  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/201,139  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/508,735  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/03316  
; FILING DATE: 17-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-109348  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4848  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; US-09-201-139-23

Query Match

23.6%; Score 6.6; DB 1; Length 16;



Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19  
Db 13 CTTCTGGACAG 1

RESULT 211  
US-09-120-131-23/c  
; Sequence 23, Application US/09120131  
; Patent No. 6218146  
; GENERAL INFORMATION:  
; APPLICANT: Ramb, Alexander  
; TITLE OF INVENTION: MTS2 GENE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/120,131  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/486,047  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: PCT/US95/03316  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/251,938  
; FILING DATE: 01-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,087  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,086  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,369  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/214,582  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Innen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-109348-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-09-120-131-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;

Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19  
Db 13 CTTCTGGACAG 1

RESULT 212  
US-08-522-384-34  
; Sequence 34, Application US/08522384  
; Patent No. 6118667  
; GENERAL INFORMATION:  
; APPLICANT: LOPEZ-NIETO, CARLOS E  
; APPLICANT: NIGAM, SANJAY KUMAR  
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR  
; CHARACTERIZING NUCLEOTIDE SEQUENCES  
; FILE REFERENCE: 2458-4029  
; CURRENT APPLICATION NUMBER: US/08/522,384  
; CURRENT FILING DATE: 1996-11-15  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE: Description of Unknown Organism: Primer  
; OTHER INFORMATION: Description of Unknown Organism: Primer  
US-08-522-384-34

Query Match 22.9%; Score 6.4; DB 1; Length 10;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CGTGTCAC 17  
Db 3 CATGTACA 10

RESULT 213  
US-09-425-798-12  
; Sequence 12, Application US/09425798A  
; Patent No. 6423493  
; GENERAL INFORMATION:  
; APPLICANT: Gorenstein Dr., David G.  
; APPLICANT: King Dr., David J.  
; APPLICANT: Ventura, Daniel A.  
; APPLICANT: Brasier Dr., Allan R.  
; TITLE OF INVENTION: Combinatorial Selection of Phosphothionate  
; FILE REFERENCE: 122144-1005  
; CURRENT APPLICATION NUMBER: US/09/425,798A  
; CURRENT FILING DATE: 1999-10-25  
; PRIOR APPLICATION NUMBER: 60/105,600  
; PRIOR FILING DATE: 1999-10-26  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: aptamer  
US-09-425-798-12

Query Match 22.9%; Score 6.4; DB 1; Length 10;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACAGG 19  
Db 3 TGTACATG 10

RESULT 214  
US-08-319-492B-24/C  
; Sequence 24, Application US/09319492B  
; Patent No. 5616488  
; GENERAL INFORMATION:  
; APPLICANT: Sullivan, Sean M.  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: RBOZTME TREATMENT OF DISEASES  
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS  
; NUMBER OF SEQUENCES: 751  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/319,492B  
; FILING DATE: October 7, 1994  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/276  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-319-492B-24

Query Match 22.1%; Score 6.2; DB 1; Length 15;  
Best Local Similarity 72.7%; Pred. No. 2e+02;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGAGTC 24  
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Db 14 TACAGTAGGC 4

RESULT 215  
US-09-989-789-2453  
; Sequence 2453, Application US/09989789  
; Patent No. 6588746  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2453  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-2453

Query Match 21.4%; Score 6; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e-02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCC 7  
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Db 3 GGGCCC 8

RESULT 216  
US-09-989-789-2454  
; Sequence 2454, Application US/09989789  
; Patent No. 6588746  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2454  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-2454

Query Match 21.4%; Score 6; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e-02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCC 7  
|||  
Db 3 GGGCCC 8

RESULT 217  
US-09-153-242-30/C  
; Sequence 30, Application US/09153242  
; Patent No. 6482592  
; GENERAL INFORMATION:  
; APPLICANT: Lundberg, Joakim  
; APPLICANT: Uhlen, Mathias  
; TITLE OF INVENTION: MODULAR PROBES II  
; FILE REFERENCE: 1181-242  
; CURRENT APPLICATION NUMBER: US/09/153,242  
; CURRENT FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: PCT/GB97/02629  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide H1-9  
US-09-153-242-30

Query Match 21.4%; Score 6; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e-02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCC 7  
Db 6 GGGCCC 1

RESULT 218

US-09-153-242-33/c  
; Sequence 33, Application US/09153242  
; Patent No. 6482592  
; GENERAL INFORMATION:  
; APPLICANT: Lundberg, Joakim  
; TITLE OF INVENTION: MODULAR PROBES II  
; FILE REFERENCE: 1181-242  
; CURRENT APPLICATION NUMBER: US/09/153,242  
; CURRENT FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: PCT/GB97/02629  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide H3  
US-09-153-242-33

Query Match 21.4%; Score 6; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e-02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCC 7  
Db 7 GGGCCC 2

Search completed: April 19, 2004, 15:06:49  
Job time : 1 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 15:10:53 ; Search time 0.001 Seconds

(without alignments)  
68.488 Million cell updates/sec

Title: US-10-024-396-3-COPY

Perfect score: 28

Sequence: 1 cgggcccacgtgtacaggaggtccagg 28

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 95 seqs, 1223 residues

Total number of hits satisfying chosen parameters: 190

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 132 summaries

Database : pbdb:\*

*Published - Applications - NA*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	71.4	20	1	US-10-024-396-19
C 2	20	71.4	20	1	US-10-024-396-20
C 3	14.2	50.7	21	1	US-08-983-605-203
C 4	14.2	50.7	21	1	US-09-853-105-19
C 5	13.4	47.9	20	1	US-09-918-779-35
C 6	13.2	47.1	20	1	US-10-159-856-39
C 7	13.2	47.1	20	1	US-10-159-856-105
C 8	12.4	44.3	19	1	US-10-184-372-23
C 9	12.2	43.6	17	1	US-09-882-945A-275
C 10	11.4	40.7	17	1	US-09-930-423-643
C 11	11.4	40.7	17	1	US-09-930-423-1045
C 12	11.4	40.7	17	1	US-09-930-423-1120
C 13	11.4	40.7	17	1	US-09-745-237A-643
C 14	11.4	40.7	17	1	US-09-745-237A-1045
C 15	11.4	40.7	17	1	US-09-745-237A-1120
C 16	11.2	40.0	17	1	US-09-818-875-2950
C 17	11.2	40.0	17	1	US-09-818-875-2951
C 18	11.2	40.0	17	1	US-10-156-308-7026
C 19	11.2	40.0	17	1	US-10-156-308-7027
C 20	11.2	40.0	17	1	US-10-238-700-3087
C 21	11.2	40.0	17	1	US-10-209-787-2950
C 22	11.2	40.0	17	1	US-10-209-787-2951
C 23	11.2	40.0	17	1	US-10-261-185-2951
C 24	11.2	40.0	17	1	US-10-261-185-2951
C 25	10.8	38.6	15	1	US-09-504-231A-143
C 26	10.8	38.6	15	1	US-09-504-231A-143
C 27	10.4	37.1	12	1	US-10-407-637-20
C 28	10.2	36.4	15	1	US-09-879-813-73
C 29	10.2	36.4	15	1	US-09-912-673A-55
C 30	10.2	36.4	15	1	US-10-146-505-73
C 31	10.2	36.4	15	1	US-10-193-507-83
C 32	10.3	35.7	10	1	US-10-193-507-83
C 33	10.3	35.7	10	1	US-09-504-231A-319
C 34	10.3	35.7	10	1	US-09-504-231A-319

34	10	35.7	15	1	US-10-193-507-51	Sequence 51, Appl
35	9.8	35.0	14	1	US-08-591-486B-61	Sequence 61, Appl
36	9.8	35.0	15	1	US-05-504-231A-137	Sequence 137, Appl
37	9.8	35.0	15	1	US-09-274-553D-137	Sequence 137, Appl
38	9.8	35.0	15	1	US-10-113-877-35	Sequence 35, Appl
39	9.4	33.6	12	1	US-09-989-364-67	Sequence 67, Appl
40	9.2	32.9	14	1	US-08-551-486B-164	Sequence 164, Appl
C 41	9	32.1	10	1	US-10-330-627-29	Sequence 29, Appl
C 42	8.8	31.4	12	1	US-09-989-364-67	Sequence 67, Appl
C 43	8.8	31.4	13	1	US-10-104-307-26	Sequence 26, Appl
C 44	8.4	30.0	10	1	US-09-851-871-85	Sequence 85, Appl
C 45	8.4	30.0	10	1	US-10-329-465-242	Sequence 242, Appl
C 46	8.4	30.0	10	1	US-10-330-627-1257	Sequence 1257, Appl
C 47	8.4	30.0	10	1	US-10-330-627-1257	Sequence 1257, Appl
C 48	8.4	30.0	10	1	US-10-444-206-85	Sequence 85, Appl
C 49	8.4	30.0	10	1	US-09-249-155-45	Sequence 45, Appl
C 50	8.4	30.0	11	1	US-09-851-871-86	Sequence 86, Appl
C 51	8.4	30.0	11	1	US-10-314-322-45	Sequence 45, Appl
C 52	8.4	30.0	11	1	US-10-444-206-86	Sequence 86, Appl
C 53	8.4	30.0	11	1	US-09-851-871-87	Sequence 87, Appl
C 54	8.4	30.0	12	1	US-10-444-206-87	Sequence 87, Appl
C 55	8.2	29.3	17	1	US-10-238-700-3087	Sequence 3087, Appl
C 56	8.2	29.3	20	1	US-10-024-396-19	Sequence 19, Appl
C 57	8.2	29.3	20	1	US-09-853-105-19	Sequence 19, Appl
C 58	8.2	29.3	21	1	US-09-989-789-2098	Sequence 2098, Appl
C 59	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 60	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 61	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 62	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 63	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 64	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 65	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 66	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 67	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 68	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 69	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 70	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 71	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 72	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 73	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 74	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 75	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 76	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 77	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 78	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 79	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 80	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 81	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 82	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 83	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 84	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 85	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 86	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 87	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 88	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 89	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 90	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 91	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 92	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 93	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 94	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 95	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 96	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 97	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 98	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 99	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 100	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 101	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 102	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 103	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 104	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 105	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl
C 106	8.2	29.3	21	1	US-09-989-789-2100	Sequence 2100, Appl

Sequence 2951, Ap  
Sequence 73, Appl  
Sequence 73, Appl  
Sequence 319, Appl  
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Sequence 105, Appl  
Sequence 105, Appl  
Sequence 275, Appl  
Sequence 19, Appl  
Sequence 164, Appl  
Sequence 203, Appl  
Sequence 643, Appl  
Sequence 1045, Ap  
Sequence 1120, Ap  
Sequence 643, Appl  
Sequence 1045, Ap  
Sequence 1120, Ap  
Sequence 176254,  
Sequence 176254,  
Sequence 20, Appl  
Sequence 2453, Ap  
Sequence 2454, Ap  
Sequence 2453, Ap  
Sequence 2454, Ap  
Sequence 2453, Ap  
Sequence 2454, Ap  
Sequence 2453, Ap  
Sequence 2454, Ap

107 7.6 27.1 17 1 US-10-261-185-2951  
108 7.2 25.7 15 1 US-09-579-813-73  
109 7.2 25.7 15 1 US-10-146-505-73  
110 7.2 25.7 15 1 US-09-504-231A-319  
111 7.2 25.7 15 1 US-09-274-553D-319  
112 7.2 25.7 20 1 US-10-159-856-39  
113 7.2 25.7 20 1 US-10-159-856-105  
114 7 25.0 17 1 US-09-882-945A-275  
115 6.8 24.3 12 1 US-09-923-507-19  
116 6.8 24.3 14 1 US-08-591-486B-164  
117 6.8 24.3 19 1 US-08-983-605-203  
118 6.6 23.6 17 1 US-09-930-423-643  
119 6.6 23.6 17 1 US-09-930-423-1045  
120 6.6 23.6 17 1 US-09-930-423-1120  
121 6.6 23.6 17 1 US-09-745-237A-643  
122 6.6 23.6 17 1 US-09-745-237A-1045  
123 6.6 23.6 17 1 US-09-745-237A-1120  
124 6.4 22.9 11 1 US-10-027-632-176254  
125 6.4 22.9 11 1 US-10-027-632-176254  
126 6.2 22.1 12 1 US-10-407-637-20  
127 6 21.4 9 1 US-09-989-789-2453  
128 6 21.4 9 1 US-09-989-789-2454  
129 6 21.4 9 1 US-09-990-186-2453  
130 6 21.4 9 1 US-09-990-186-2454  
131 6 21.4 9 1 US-09-989-994-2453  
132 6 21.4 9 1 US-09-989-994-2454

ALIGNMENTS

RESULT 1  
US-10-024-396-19/c  
; Sequence 19, Application US/10024396  
; Publication No. US20030147864A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION  
; FILE REFERENCE: RTS-0339  
; CURRENT APPLICATION NUMBER: US/10/024,396  
; CURRENT FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 91  
; SEQ ID NO 19  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-024-396-19

Query Match 71.4%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCCTACGTGTACAGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 20 CGGGCCCTACGTGTACAGG 1

RESULT 2  
US-10-024-396-20/c  
; Sequence 20, Application US/10024396  
; Publication No. US20030147864A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION  
; FILE REFERENCE: RTS-0339  
; CURRENT APPLICATION NUMBER: US/10/024,396  
; CURRENT FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 91  
; SEQ ID NO 20  
; LENGTH: 20  
; TYPE: DNA

Query Match 71.4%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCCTACGTGTACAGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 20 CGGGCCCTACGTGTACAGG 1

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-024-396-20

Query Match 71.4%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGAGTCCAGG 28  
| | | | | | | | | | | | | | | | | | | | | |  
Db 20 ACGTGTACAGGAGTCCAGG 1

RESULT 3  
US-08-983-605-203/c  
; Sequence 203, Application US/08983605A  
; Publication No. US20020066118A1  
; GENERAL INFORMATION:  
; APPLICANT: Roder, Marion  
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species  
; TITLE OF INVENTION: Triticum Aestivum and Tribe Triticeae and the Use of  
; TITLE OF INVENTION: Said Markers  
; FILE REFERENCE: 2936.10400  
; CURRENT APPLICATION NUMBER: US/08/983,605A  
; CURRENT FILING DATE: 1998-05-01  
; EARLIER APPLICATION NUMBER: DE 195 25 284.5  
; EARLIER FILING DATE: 1995-06-28  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 203  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
US-08-983-605-203

Query Match 50.7%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 5;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCCTACGTGTACAGGGAG 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 19 GCCTTAGCGGTACAGGGAG 1

RESULT 4  
US-09-853-105-19  
; Sequence 19, Application US/09853105  
; Publication No. US20030149236A1  
; GENERAL INFORMATION:  
; APPLICANT: Hilton, Douglas J.  
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/853,105  
; FILING DATE: 10-May-2001  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/702,665  
; FILING DATE: 20-DEC-1996  
; ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold  
REGISTRATION NUMBER: 19,827  
REFERENCE/DOCKET NUMBER: 10296  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 203 901 SANS UR  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-853-105-19

Query Match 50.7%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 6.1;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCCAGG 28  
Db 3 CCTGACTGGAGTCCAGG 21

## RESULT 5

US-09-918-779-35/C  
Sequence 35, Application US/09918779  
Publication No. US20030064369A1

GENERAL INFORMATION:  
APPLICANT: Taupier, Raymond  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Rastelli, Luca  
APPLICANT: Spaderma, Steven  
APPLICANT: Shinkets, Richard  
APPLICANT: Zerhusen, Bryan  
APPLICANT: Spytek, Kimberly  
APPLICANT: Shency, Suresh  
APPLICANT: Li, Li  
APPLICANT: Gusev, Vladimir  
APPLICANT: Grosse, William  
APPLICANT: Alsobrook, John  
APPLICANT: Lepley, Denise  
APPLICANT: Burgess, Catherine  
APPLICANT: Gerlach, Valerie  
APPLICANT: Ellerman, Karen  
APPLICANT: MacDougall, John  
APPLICANT: Stone, David  
APPLICANT: Smithson, Glenda  
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-074 US  
CURRENT APPLICATION NUMBER: US/09/918,779  
CURRENT FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/221,409  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: 60/222,840  
PRIOR FILING DATE: 2000-08-04  
PRIOR APPLICATION NUMBER: 60/223,752  
PRIOR FILING DATE: 2000-08-08  
PRIOR APPLICATION NUMBER: 60/223,762  
PRIOR FILING DATE: 2000-08-08  
PRIOR APPLICATION NUMBER: 60/223,770  
PRIOR FILING DATE: 2000-08-08  
PRIOR APPLICATION NUMBER: 60/223,769  
PRIOR FILING DATE: 2000-08-08  
PRIOR APPLICATION NUMBER: 60/225,146  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/225,392  
PRIOR FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: 60/225,470  
PRIOR FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: 60/225,697

PRIOR FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: 60/263,662  
PRIOR FILING DATE: 2001-02-01  
PRIOR APPLICATION NUMBER: 60/281,645  
PRIOR FILING DATE: 2001-04-05  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 35  
LENGTH: 20  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide  
OTHER INFORMATION: primers  
US-09-918-779-35

Query Match 47.9%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 8.5;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 TACAGGAGTCCAGG 28  
Db 17 TAGAGGAGTCCAGG 3

## RESULT 6

US-10-159-856-39/C  
Sequence 39, Application US/10159856  
Publication No. US2003022869A1

GENERAL INFORMATION:  
APPLICANT: Susan M. Freier  
APPLICANT: Kenneth W. Dobie  
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPI  
FILE REFERENCE: RTS-0365  
CURRENT APPLICATION NUMBER: US/10/159,856  
CURRENT FILING DATE: 2002-05-31  
NUMBER OF SEQ ID NOS: 134  
SEQ ID NO 39  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-159-856-39

Query Match 47.1%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.4;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCCTAGTGTACAGGA 21  
Db 19 GCGCATCGTGTACAGGA 2

## RESULT 7

US-10-159-856-105  
Sequence 105, Application US/10159856  
Publication No. US2003022869A1

GENERAL INFORMATION:  
APPLICANT: Susan M. Freier  
APPLICANT: Kenneth W. Dobie  
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPI  
FILE REFERENCE: RTS-0365  
CURRENT APPLICATION NUMBER: US/10/159,856  
CURRENT FILING DATE: 2002-05-31  
NUMBER OF SEQ ID NOS: 134  
SEQ ID NO 105  
LENGTH: 20  
TYPE: DNA  
ORGANISM: H. sapiens  
FEATURE:  
US-10-159-856-105

```
Query Match      47.1%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  4  GCGCTACGTGTACAGGGA 21
DB  2  GCGCATCGTGTACAGGGA 19

RESULT 8
US-10-184-372-23
; Sequence 23, Application US/10184372
; Publication No. US20030219852A1
; GENERAL INFORMATION:
; APPLICANT: Bank, Rudolf A.
; APPLICANT: Van der Slot, Annemarie J.
; APPLICANT: Zuurmond, Anne-Marie
; APPLICANT: Te Koppelaar, Johannes M.
; TITLE OF INVENTION: Modification of collagenous materials and medical treatment, diag
; TITLE OF INVENTION: and monitoring of fibrotic conditions
; FILE REFERENCE: P60187US00
; CURRENT APPLICATION NUMBER: US/10/184,372
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 09/450,209
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-184-372-23

Query Match      44.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 13;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  15  ACAGGGAGTCCAGG 28
DB  3  ACAGGGATCCAGG 16

RESULT 9
US-09-882-945A-275
; Sequence 275, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 275
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-275

Query Match      43.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 12;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2  GGSCCTACGTGTACAG 18
```

```
DB  1  GGACCTATGTCTACAG 17

RESULT 10
US-09-930-423-643/c
; Sequence 643, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A,400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 643
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-643

Query Match      40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  11  GTGTACAGCGAGT 23
DB  15  GTGTACAGCGAGT 3

RESULT 11
US-09-930-423-1045/c
; Sequence 1045, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A,400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1045
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1045

Query Match      40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  11  GTGTACAGCGAGT 23
DB  17  GTGTACAGCGAGT 5

RESULT 12
US-09-930-423-1120/c
; Sequence 1120, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A,400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
```

```
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1120
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1120

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGT 23
Db 14 GTGTACAGGAGT 2

RESULT 13
US-09-745-237A-643/c
; Sequence 643, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 643
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-643

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGT 23
Db 15 GTGTACAGGAGT 3

RESULT 14
US-09-745-237A-1045/c
; Sequence 1045, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1045
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1045

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGT 23
Db 11 GTGTACAGGAGT 23

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGT 23
Db 14 GTGTACAGGAGT 2

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGT 23
Db 14 GTGTACAGGAGT 2
```

```
Db 17 GTGTACAGGAGT 5

RESULT 15
US-09-745-237A-1120/c
; Sequence 1120, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1120
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1120

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGT 23
Db 14 GTGTACAGGAGT 2

RESULT 16
US-09-818-875-2950/c
; Sequence 2950, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gampfer, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: 400/007 (MHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2950
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-2950

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 20;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGAGTC 24
Db 17 ACTGTCCAGGAGGC 2

RESULT 17
US-09-818-875-2951
; Sequence 2951, Application US/09818875
```



```

; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US/09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-818-875-2951

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 20;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGAGTC 24
   |||||
Db 1 ACTTGTCCAGGAGGC 16

RESULT 18
US-10-156-306-7026
; Sequence 7026, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MEBH01-664-A (400/050)
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7026
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-156-306-7026

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 20;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGGAGTCACG 27
   :|||
Db 2 UGCAGAGGAGUACAG 17

RESULT 19
US-10-156-306-7027
; Sequence 7027, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MEBH01-664-A (400/050)
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7027
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-156-306-7027

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 20;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGGAGTCACG 27
   :|||
Db 1 UGCAGAGGAGUACAG 16

RESULT 20
US-10-238-700-3087
; Sequence 3087, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Lev
; FILE REFERENCE: 400/057 (MEBH01-1158-A)
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3087
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-238-700-3087

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGGAG 22
   |||
Db 1 CCACCAGUACAGGAG 16

RESULT 21
US-10-209-787-2950/c
; Sequence 2950, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/10/209,787
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01

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```
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2950
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-2950

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 20;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      9 ACGTGTACAGGAGTC 24
        |||||
Db      17 ACTTGTCAGGAGGC 2

RESULT 22
US-10-209-787-2951
; Sequence 2951, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-2951

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 20;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      9 ACGTGTACAGGAGTC 24
        |||||
Db      1 ACTTGTCAGGAGGC 16

RESULT 23
US-10-261-185-2950/c
; Sequence 2950, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-2951

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 20;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      9 ACGTGTACAGGAGTC 24
        |||||
Db      1 ACTTGTCAGGAGGC 16

RESULT 24
US-10-261-185-2951
; Sequence 2951, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-2951

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 20;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      9 ACGTGTACAGGAGTC 24
        |||||
Db      1 ACTTGTCAGGAGGC 16

RESULT 25
US-09-504-231A-143
; Sequence 143, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
```

APPLICANT: Roberts, Beth  
APPLICANT: Pavco, Pamela  
APPLICANT: Macejak, Dennis  
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
FILE REFERENCE: fpi 247/282  
CURRENT APPLICATION NUMBER: US/09/504,231A  
CURRENT FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: 09/274,553  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 09/257,608  
PRIOR FILING DATE: 1999-02-24  
PRIOR APPLICATION NUMBER: 60/100,842  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/083,217  
PRIOR FILING DATE: 1998-04-27  
NUMBER OF SEQ ID NOS: 3.0  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 143  
LENGTH: 15  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-143

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 19;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15  
|||||: |||:  
Db 1 GGGCCCUCCGUGCA 14

RESULT 26  
US-09-274-553D-143  
Sequence 143, Application US/09274553D  
Patent No. US2002008225A1  
GENERAL INFORMATION:  
APPLICANT: Macejak, Dennis  
APPLICANT: Pavco, Pamela  
APPLICANT: Macejak, Dennis  
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
FILE REFERENCE: fpi 247/282  
CURRENT APPLICATION NUMBER: US/09/274,553D  
CURRENT FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 09/257,608  
PRIOR FILING DATE: 1999-02-24  
PRIOR APPLICATION NUMBER: 60/100,842  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/083,217  
PRIOR FILING DATE: 1998-04-27  
NUMBER OF SEQ ID NOS: 3.0  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 143  
LENGTH: 15  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-274-553D-143

Query Match 38.6%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 19;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15  
|||||: |||:  
Db 1 GGGCCCUCCGUGCA 14

RESULT 27  
US-10-407-637-20/c  
Sequence 20, Application US/10407637  
Publication No. US20030194736A1  
GENERAL INFORMATION:  
APPLICANT: Bitinaite, Jurate  
TITLE OF INVENTION: Methods And Compositions For DNA Manipulation  
FILE REFERENCE: NEB-203-US  
CURRENT APPLICATION NUMBER: US/10/407,637  
CURRENT FILING DATE: 2003-04-04  
PRIOR APPLICATION NUMBER: US 60/372,352  
PRIOR FILING DATE: 2002-04-12  
PRIOR APPLICATION NUMBER: US 60/372,675  
PRIOR FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: US 60/421,010  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 20  
LENGTH: 12  
TYPE: DNA  
ORGANISM: unknown  
FEATURE:  
OTHER INFORMATION: mutated pUC19  
US-10-407-637-20

Query Match 37.1%; Score 10.4; DB 1; Length 12;  
Best Local Similarity 91.7%; Pred. No. 15;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCTACGTGTACA 17  
|||||: |||:  
Db 12 CCTAGGTGTACA 1

RESULT 28  
US-09-879-813-73/c  
Sequence 73, Application US/09879813  
Patent No. US20020155453A1  
GENERAL INFORMATION:  
APPLICANT: Neuberger, Michael S.  
APPLICANT: Cumbers, Sarah J.  
TITLE OF INVENTION: Method of Generating Diversity  
FILE REFERENCE: 18396/2005  
CURRENT APPLICATION NUMBER: US/09/879,813  
CURRENT FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: 09/828,717  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: PCT/GB99/03358  
PRIOR FILING DATE: 1999-10-08  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 73  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (7)..(10)  
OTHER INFORMATION: F264  
OTHER INFORMATION: The sequence ACA replaces the sequence GAGAG.46bp.CGTC  
US-09-879-813-73

Query Match 36.4%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 26;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCCTACGTGTACAG 18  
|||||: |||:  
Db 15 GCCCATGTGCACAG 1

RESULT 29  
US-09-912-673A-55/c  
; Sequence 55, Application US/09912673A  
; Publication No. US2003018230A1  
; GENERAL INFORMATION:  
; APPLICANT: Ye, Bangce  
; TITLE OF INVENTION: MEDIUM AND LOW DENSITY GENE CHIPS  
; FILE REFERENCE: JNB 100  
; CURRENT APPLICATION NUMBER: US/09/912,673A  
; CURRENT FILING DATE: 2001-07-23  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 55  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: P(qs)1 DNA probe  
US-09-912-673A-55

Query Match 36.4%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 26;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGTGTACAGGGAGTC 24  
DB 15 CTGTCCAGGGAGGC 1

RESULT 30  
US-10-146-505-73/c  
; Sequence 73, Application US/10146505  
; Publication No. US20030108869A1  
; GENERAL INFORMATION:  
; APPLICANT: Neuberger, Michael S.  
; APPLICANT: Cumbers, Sarah J.  
; TITLE OF INVENTION: Method of Generating Diversity  
; FILE REFERENCE: 18396/2005B  
; CURRENT APPLICATION NUMBER: US/10/146,505  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/828,717  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 09/879,813  
; PRIOR FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: PCT/GB99/03358  
; PRIOR FILING DATE: 1999-10-08  
; PRIOR APPLICATION NUMBER: GB 9822104.7  
; PRIOR FILING DATE: 1998-10-09  
; PRIOR APPLICATION NUMBER: GB 9901141.3  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: GB 9913435.5  
; PRIOR FILING DATE: 1999-06-09  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 73  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; LOCATION: (7)..(10)  
; OTHER INFORMATION: F264  
; OTHER INFORMATION: The sequence ACA replaces the sequence GAGAG.46bp.CGTC  
US-10-146-505-73

Query Match 36.4%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 26;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCTACGTGTACAG 18

Db 15 GCCCATGTGCACAG 1  
RESULT 31  
US-10-193-507-83  
; Sequence 83, Application US/10193507  
; Publication No. US20040018493A1  
; GENERAL INFORMATION:  
; APPLICANT: Anastasio, Alison E.  
; APPLICANT: Kazemi, Amir  
; APPLICANT: Lachowicz, Michael F.  
; APPLICANT: Pabon, Vicente  
; APPLICANT: Shah, Nisha  
; TITLE OF INVENTION: HAPLOTYPES OF THE CD3E GENE  
; FILE REFERENCE: MMH-2790US  
; CURRENT APPLICATION NUMBER: US/10/193,507  
; CURRENT FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: 60/304,573  
; PRIOR FILING DATE: 2001-07-11  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 83  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-193-507-83

Query Match 35.7%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAGTC 24  
DB 1 ACAGGGAGTC 10

RESULT 32  
US-09-504-231A-319  
; Sequence 319, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELA  
; FILE REFERENCE: FDI 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 319  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-319

Query Match 35.7%; Score 10; DB 1; Length 15;  
Best Local Similarity 90.0%; Pred. No. 29;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28  
||||:|||||  
Db 3 GGAGUCCAGG 12

## RESULT 33

US-09-274-553D-319  
; Sequence 319, Application US/09274553D  
; Patent No. US2002008225A1

## ; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: MacGjak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

; FILE REFERENCE: IPI 247/282

; CURRENT APPLICATION NUMBER: US/09/274,553D

; CURRENT FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3148

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 319

; LENGTH: 15

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-274-553D-319

Query Match 35.7%; Score 10; DB 1; Length 15;  
Best Local Similarity 90.0%; Pred. No. 29;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28  
||||:|||||  
Db 3 GGAGUCCAGG 12

## RESULT 34

US-10-193-507-51

; Sequence 51, Application US/10193507

; Publication No. US20040018493A1

## ; GENERAL INFORMATION:

; APPLICANT: Anastasio, Alison E.

; APPLICANT: Kazemi, Amir

; APPLICANT: Lachowicz, Michael F.

; APPLICANT: Pabon, Vicente

; APPLICANT: Shah, Nisha

; TITLE OF INVENTION: HAPLOTYPES OF THE CD3E GENE

; FILE REFERENCE: MWH-2790US

; CURRENT APPLICATION NUMBER: US/10/193,507

; CURRENT FILING DATE: 2002-07-12

; PRIOR APPLICATION NUMBER: 60/304,573

; PRIOR FILING DATE: 2001-07-11

; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 51

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-193-507-51

Query Match 35.7%; Score 10; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAGTC 24  
||||:|||||  
Db 4 ACAGGGAGTC 13

## RESULT 35

US-08-591-486B-61

; Sequence 61, Application US/08591486B

; Publication No. US20020037866A1

## ; GENERAL INFORMATION:

; APPLICANT: Schlengersiepen, Georg F

; APPLICANT: Schlengersiepen, Reimar

; APPLICANT: Schlengersiepen, Karl-Hermann

; APPLICANT: Gottingen, Wolfgang Brysch

; TITLE OF INVENTION: A Pharmaceutical Composition

; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treat

; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the

; TITLE OF INVENTION: Treatment of Neoplasms

; NUMBER OF SEQUENCES: 185

; CORRESPONDENCE ADDRESS: 185

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh Street, N.W.

; CITY: Washington, D.C

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/591,486B

; FILING DATE: 11-JAN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93111059.7

; FILING DATE: 10-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP94/02218

; FILING DATE: 6-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Player, William E.

; REGISTRATION NUMBER: 31,409

; REFERENCE/DOCKET NUMBER: 10496/P60122

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 638-6666

; TELEFAX: (202) 393-9350

; TELEX: RCA 248593 IDEA UR

; INFORMATION FOR SEQ ID NO: 61:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

; ANTI-SENSE: YES

US-08-591-486B-61

Query Match 35.0%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 28;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGGTGACAGGAG 22  
||||:|||||  
Db 2 CGGTGACAGGAG 14

## RESULT 36

US-09-504-231A-137

; Sequence 137, Application US/09504231A

; Patent No. US20020013458A1

## ; GENERAL INFORMATION:

```
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 137
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-137

Query Match          35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      3  GGCCCTACGTGTA 15
Db      2  GGCCCUACGUUA 14
      |||:||||:|

RESULT 37
US-09-274-553D-137
; Sequence 137, Application US/09274553D
; Patent No. US2002008225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 137
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-137

Query Match          35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      3  GGCCCTACGTGTA 15
Db      2  GGCCCUACGUUA 14
      |||:||||:|

RESULT 38
US-10-113-877-35
; Sequence 35, Application US/10113877
; Publication No. US20020177218A1
; GENERAL INFORMATION:
; APPLICANT: Pang, Yu
; APPLICANT: Wang, Xiao-Yang
; APPLICANT: Turpin, Pierre
; TITLE OF INVENTION: Methods of detecting multiple DNA
; TITLE OF INVENTION: Binding protein and DNA interactions in a sample, and
; TITLE OF INVENTION: devices, systems and kits for practicing the same.
; FILE REFERENCE: CLON-071
; CURRENT APPLICATION NUMBER: US/10/113,877
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 60/280,658
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/314,330
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-113-877-35

Query Match          35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 32;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13  GTACAGGGAGTCC 25
Db      2  GTACAGGGGTGTC 14
      |||||:|||||

RESULT 39
US-09-989-364-67
; Sequence 67, Application US/09989364
; Publication No. US2003003463A1
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/989,364
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/203,231
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-989-364-67

Query Match          33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  CCTACGTGTAC 16
Db      2  CCTACCTGTAC 12
      |||||:|||||
```

QY 3 GGCCCTACGTGTA 15

```

RESULT 40
US-08-591-486B-164/c
; Sequence 164, Application US/08591486B
; Publication No. US20020037866A1
; GENERAL INFORMATION:
; APPLICANT: Schlingsiepen, Georg F
; APPLICANT: Schlingsiepen, Reimar
; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Göttingen, Wolfgang Brysch
; TITLE OF INVENTION: A Pharmaceutical Composition
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatm
; TITLE OF INVENTION: Of Neuronal Injury, Degeneration and Cell Death and for the
; TITLE OF INVENTION: Treatment of Neoplasms
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,486B
; FILING DATE: 11-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93111059.7
; FILING DATE: 10-JUL-1993
; PRIOR APPLICATION DATA: PCT/EP94/02218
; FILING DATE: 6-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10496/P60122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-9350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-591-486B-164

Query Match 32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 38;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CCTACGTGTACAGG 19
Db 14 CCTCTGTATACAGG 1

RESULT 41
US-10-330-627-29
; Sequence 29, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes

```

```

; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-29

Query Match 32.1%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GAGTCCAGG 28
Db 2 GAGTCCAGG 10

RESULT 42
US-09-989-364-67/c
; Sequence 67, Application US/09989364
; Publication No. US20030003463A1
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/989,364
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/203,231
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-989-364-67

Query Match 31.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGGAGTC 24
Db 12 GTACAGGTAGGC 1

RESULT 43
US-10-104-307-26
; Sequence 26, Application US/10104307
; Publication No. US20030180729A1
; GENERAL INFORMATION:
; APPLICANT: GUNNING, Kerry B.
; APPLICANT: POWDRILL, Tom
; APPLICANT: HOGAN, Michael
; TITLE OF INVENTION: Hybridization Rate Enhancement for Substrate-Bound Specific Nuc
; TITLE OF INVENTION: Binding Agents
; FILE REFERENCE: 053960.0001/AUS
; CURRENT APPLICATION NUMBER: US/10/104,307
; CURRENT FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 13

```

```
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)-(13)
/ OTHER INFORMATION: synthetic oligonucleotide
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: 5' amine modification
US-10-104-307-26
```

```
Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 12 TGTACAGGGAGT 23
    |||||
Db 2 TGTACAGGGCGT 13
```

## RESULT 44

```
US-09-851-871-85/c
/ Sequence 85, Application US/09851871
/ Publication No. US20030176374A1
/ GENERAL INFORMATION:
/ APPLICANT: Bennett, Clarence Frank
/ APPLICANT: Vickers, Timothy A.
/ APPLICANT: Karras, James G.
/ TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
/ FILE REFERENCE: ISPH-0543
/ CURRENT APPLICATION NUMBER: US/09/851,871
/ PRIOR FILING DATE: 2001-05-09
/ PRIOR APPLICATION NUMBER: PCT/US00/14471
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 09/326,186
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: 08/777,266
/ PRIOR FILING DATE: 1996-12-31
/ NUMBER OF SEQ ID NOS: 284
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 85
/ LENGTH: 10
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-09-851-871-85
```

```
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 13 GTACAGGGAG 22
    |||||
Db 10 GTACGGGGAG 1
```

## RESULT 45

```
US-10-329-465-242/c
/ Sequence 242, Application US/10329465
/ Publication No. US20030165949A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang et al.
/ TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLI-
/ FILE REFERENCE: 27373/37928A
/ CURRENT APPLICATION NUMBER: US/10/329,465
/ CURRENT FILING DATE: 2002-12-23
/ PRIOR APPLICATION NUMBER: US 60/343,826
/ PRIOR FILING DATE: 2001-12-27
/ NUMBER OF SEQ ID NOS: 315
/ SOFTWARE: PatentIn version 3.1
```

```
/ SEQ ID NO 242
/ LENGTH: 10
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-242
```

```
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 12 TGTACAGGGA 21
    |||||
Db 10 TGTACGGGGA 1
```

## RESULT 46

```
US-10-390-045-14
/ Sequence 14, Application US/10390045
/ Publication No. US20030170713A1
/ GENERAL INFORMATION:
/ APPLICANT: SRIVASTAVA, SHIV
/ APPLICANT: MOUL, JUDD W.
/ APPLICANT: XU, LINDA L.
/ APPLICANT: SEGAWA, TAKEHIKO
/ TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
/ FILE REFERENCE: 04995.0057-00000
/ CURRENT APPLICATION NUMBER: US/10/390,045
/ CURRENT FILING DATE: 2003-03-18
/ PRIOR APPLICATION NUMBER: US/09/769,482
/ PRIOR FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/178,772
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: 60/179,045
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 67
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 10
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: oligonucleotide
US-10-390-045-14
```

```
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 13 GTACAGGGAG 22
    |||||
Db 1 GTGCAGGGAG 10
```

## RESULT 47

```
US-10-330-627-1257/c
/ Sequence 1257, Application US/10330627
/ Publication No. US20030175771A1
/ GENERAL INFORMATION:
/ APPLICANT: Velculescu, Victor E.
/ APPLICANT: Kinzler, Kenneth W.
/ APPLICANT: Vogelstein, Bert
/ TITLE OF INVENTION: Human Transcriptomes
/ FILE REFERENCE: 001107.00319
/ CURRENT APPLICATION NUMBER: US/10/330,627
/ CURRENT FILING DATE: 2002-12-30
/ PRIOR APPLICATION NUMBER: US 09/448,480
/ PRIOR FILING DATE: 1999-11-24
/ NUMBER OF SEQ ID NOS: 1584
/ SOFTWARE: FastSeq for Windows Version 4.0
```